

November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:04:19 ; Search time 14446 Seconds  
(without alignments)  
11509.559 Million cell updates/sec

Title: US-10-736-318-22  
Perfect score: 2925  
Sequence: 1 gttgttgattattgattgc.....tcaattggactaaatctg 2925

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_ey.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2835.2	96.9	103904	15	ATAC021640
2	1300.8	44.5	2294	15	AF105034
3	926.8	31.7	3004	15	AF069468
4	464.2	15.9	1163	15	AY088527
5	461	15.8	1175	6	AR608874
6	461	15.8	1175	6	AX573146
7	461	15.8	1175	15	AF099969
8	428.2	14.6	1113	15	AX176721
9	347.2	11.9	846	6	AX505726
10	228.2	7.8	1104	15	AR231157
11	228	7.8	1155	15	AF081794
12	218.8	7.5	1148	15	AF099969
13	203.4	7.0	1447	6	AR237880
14	188	6.4	1210	6	AR237881
15	188	6.4	1210	15	BT009523
16	187	6.4	911	6	AR237878
17	184.8	6.3	1189	15	BT016653
18	179.6	6.1	1253	15	AK111908

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20	176.4	6.0	1242	15	AK112014	AK112014	Oryza sat	
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26	138.8	4.7	446	6	BD273096	BD273096	Materials	
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ALIGNMENTS

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LOCUS Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence,  
DEFINITION complete sequence.  
ACCESSION AC021640  
VERSION AC021640  
KEYWORDS HTG.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 103904)  
Lin.X., Kaul.S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.,  
Wu.D., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,  
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.  
Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence  
Unpublished  
2 (bases 1 to 103904)  
Lin.X. and Kaul,S.  
Direct Submission  
Submitted (18-JAN-2000) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA, xlin@tigr.org  
3 (bases 1 to 103904)  
Lin.X.  
Direct Submission  
Submitted (24-JAN-2001) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA  
On Jan 24, 2001 this sequence version replaced gi:12280770.  
Address all correspondence to:at@tigr.org

BAC clone F16B3 is from Arabidopsis chromosome III and is near the  
molecular marker mi74.  
The orientation of the sequence is from SP6 to T7 end of the BAC  
clone.  
Genes were identified by a combination of three methods: Gene  
prediction programs including GRAIL (available by anonymous ftp  
from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of  
Washington), Genscan (Chris Burge,  
http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene



[illegible]



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Db 2008 CCCCATAATTCAGAGATCTCACCAATCAAATGCTGGCTGG-CCCCATATATAGATGGGC 2066  
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LOCUS Arabidopsis thaliana sterol-C5-desaturase gene, complete cds.  
DEFINITION AF069468  
ACCESSION AF069468  
VERSION AF069468.1 GI:4234767  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
REFERENCE 1 (bases 1 to 3004)  
AUTHORS Huselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.  
TITLE Delta7-sterol-C5-desaturase: molecular characterization and  
functional expression of wild-type and mutant alleles  
JOURNAL Plant Mol. Biol. 39 (5), 891-906 (1999)  
PUBMED 10344195  
REFERENCE 2 (bases 1 to 3004)  
AUTHORS Huselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAY-1998) IBMP, 28, rue Goethe, Strasbourg 67083,  
France  
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Location/Qualifiers  
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FKAB"  
CDS  
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Best Local Similarity 99.5%; Pred. No. 1.2e-163;  
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Db 2029 GTTTGGTATTATTGGATGACAGAGAGCTTCATGACATTAAGCCTCTCTATAAGTATCT 2088  
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QY 181 AAAAGACTTTGTGACGAGCTGTTGATCTCAAATACATTTTGCATTCCTTATCATAA 240



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Qy	361	GGAAATGACGAGAAAGTTCTTTTATCTACTTCTGAGTGTATCTTGGTGTAAATCCAAAGA	420
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Qy	480	ACCAGTAGACGGGATCTTAAAGGCTGTACCGCATGTGATAGGCGCTG-TTATAGTGCCTAA	538
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Qy	599	ATGACTGCATCCATGCGCAACATCTGCGCATGTGATAGGCGCGATATGAGCGCGAAATCC	658
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Qy	659	ACAGCATACAAAGCATAACTATGGTCAATATACCATATGATGAGTGGATGTTTGGCT	718
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Qy	959	GCAAGA 964	
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DEFINITION	Arabidopsis thaliana clone 7564 mRNA, complete sequence.
ACCESSION	AY088527
VERSION	AY088527.1 GI:21407301
KEYWORDS	FLI CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	1 (bases 1 to 1163)
AUTHORS	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE	Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)

12093376	
2 (bases 1 to 1163)	
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.	
Full-length cDNA from Arabidopsis thaliana	
Unpublished	
3 (bases 1 to 1163)	
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.	
Direct Submission	
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA	
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.	
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Best Local Similarity 99.0%; Pred. No. 8.3e-77;	
Matches 488; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	
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Db 671 TTTGGCGGCTTGCAATTTCAACAGTAGACGGGATACCTTCAGGCTGTACCGCATGTGATA 730	
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RESULT 5
AR608874
LOCUS AR608874 1175 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 23 from patent US 6822142.
ACCESSION AR608874
VERSION AR608874.1 GI:56663610
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Karunanandaa, B., Post-Beittenmiller, M., Venkatramesh, M.,
Kishore, G.M., Thorne, G.M. and LeDeaux, J.R.
TITLE Transgenic plants containing altered levels of steroid compounds
JOURNAL Patent: US 6822142-A 23 23-NOV-2004;
Monsanto Company; St. Louis, MO
FEATURES
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1. .1175
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Best Local Similarity 97.6%; Pred. No. 3.3e-76;
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Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCCTTCTGTGTTCTTTTCTTTCTTTCTTTCTTTTCAATGT 1062
Qy 880 GTCTCTCTCAACCTTTCCAAATTATATGTTATGTTACAAACATTTGCTGTCTAGTTTAAACATG 939
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Qy 940 TAAATGTTTGATGATCTTTGC 960
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RESULT 6
AX573146
LOCUS AX573146 1175 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 23 from Patent WO2061072.
ACCESSION AX573146
VERSION AX573146.1 GI:26005070
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.s.
REFERENCE
AUTHORS Karunanandaa, B., Post-Beittenmiller, M., Venkatramesh, M.,
Kishore, G.M., Thorne, G.M. and LeDeaux, J.
TITLE Transgenic plants containing altered levels of steroid compounds
JOURNAL Patent: WO 02061072-A 23 08-AUG-2002;
Monsanto Technology LLC (US)
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1. .1175
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Query Match 15.8%; Score 461; DB 6; Length 1175;
Best Local Similarity 97.6%; Pred. No. 3.3e-76;
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
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Db 643 TTTGCGGGCTTGCAATTTCCACCAGTAGAGGGGATCTTCAAGCTGTACCGCATGTGATA 702
Qy 521 GCGCTG-TTATAGTGCCAAATTCATTTCAACATCATATAGGTCCTTTTGTTCATGGAAGCG 579
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Qy 940 TAAATGTTTGATGATCTTTGC 960
Db 1123 TAAATGTTTGATGATCTTTCC 1143

RESULT 7
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LOCUS	ATRNASC5D	1175 bp	mRNA	linear	PLN 13-FEB-1997
DEFINITION	A.thaliana mRNA for sterol-C5-desaturase.				
ACCESSION	X90454				
VERSION	X90454.1	GI:1061037			
KEYWORDS	sterol-C5-desaturase gene.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1				
AUTHORS	Gachotte,D., Husselstein,T., Bard,M., Lacroute,F. and Benveniste,P.				
TITLE	Isolation and characterization of an Arabidopsis thaliana cDNA encoding a delta 7-sterol-C-5-desaturase by functional complementation of a defective yeast mutant				
JOURNAL	Plant J. 9 (3), 391-398 (1996)				
PUBMED	8919915				
REFERENCE	2 (bases 1 to 1175)				
AUTHORS	Gachotte,D.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-JUL-1995) D. Gachotte, Institut de Biologie Moleculaire Plantes, Enzymologie Moleculaire et Cellulaire, Institut de botanique 28, rue Goethe, F- 67083 Strasbourg, FRANCE				
FEATURES	Location/Qualifiers				
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CDS					
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	Arabidopsis thaliana mRNA for sterol-C5-desaturase, complete cds,				
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ACCESSION	AKI76721				
VERSION	AKI76721.1				
KEYWORDS	FLI CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1				
AUTHORS	Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K., Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.				
TITLE	Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1113)				
AUTHORS	Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K., Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@gs.riken.jp, URL:http://range.gsc.riken.jp/, Tel:81-45-503-9625, Fax:81-45-503-9586)				
COMMENT	An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://range.gsc.riken.jp/) for further details.				
FEATURES	Location/Qualifiers				
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2453 TATACGCGACGTATAGCGCTGTTTATAGTGGCGATTTCATCTCATCAACAATCTGAGTCT 2512  
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2693 AG 2694  
903 TG 904

RESULT 12  
AF099969  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AF099969 1148 bp mRNA linear PLN 19-MAY-1999  
Nicotiana tabacum sterol-C5(6)-desaturase homolog mRNA, complete cds.  
AF099969  
AF099969.1 GI:4426626  
Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 1148)  
Hussein, T., Schaller, H., Gachotte, D. and Benveniste, P.  
Delta7-sterol-C5-desaturase: molecular characterization and  
functional expression of wild-type and mutant alleles  
Plant Mol. Biol. 39 (5), 891-906 (1999)  
10344195  
2 (bases 1 to 1148)  
Benveniste, P.  
Direct Submission  
Submitted (20-OCT-1998) Plant Molecular Biology Institute,  
C.N.R.S., 28 rue Goethe, Strasbourg 67083, France  
1. .1148  
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ORIGIN

Query Match 7.5%; Score 218.8; DB 15; Length 1148;  
Best Local Similarity 61.8%; Pred. No. 8.4e-31;  
Matches 418; Conservative 0; Mismatches 172; Indels 86; Gaps 1;

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342 AGATGCCATCCCTTCAAATAGAGCTATGCTCTTGCAAATAGAGTTGCCATGAAGCTAT 401  
2082 GCCTTGGTACACTCTCTTCCAGCTGCTCTCAGATATATGATCGAGCATGGTTGGACCAA 2141  
402 GCCATTTTATGCTGCTCTTCCGCTCACTTCTGAGTATATGATTGAAATGGGTGGACAA 461  
2142 ATGTTACTCTACACTTGACCAATTTCAAAGCTGTTTCTCTCTCTCTCTCTCTCTCTCTA 2201  
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2202 TCTGTTTATGATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTT 2261  
522 TTTGGTAAATAGTAGAATTCGGCATTTATCTGGATGATCGGAGTTGCGATGACATAAACT 581  
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676 ATACTGCGAGGAGTGCCACATGATAGTACTCTTTTCTGTTGCTTGAAACATTTTACGACA 735  
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2622 CATTAATGCTCATTTATACCATATGATGATGATGATGATGATGATGATGATGATGAT 2681  
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RESULT 13  
AR237880  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AR237880 1447 bp DNA linear PAT 20-DEC-2002  
Sequence 27 from patent US 6455717.  
AR237880  
AR237880.1 GI:27282713  
Unknown.  
Unclassified.  
1 (bases 1 to 1447)  
Famodu, O.O. and Rafalski, J.A.

TITLE Sterol metabolism enzymes									
JOURNAL Patent: US 6465717-A 27 15-OCT-2002;									
E. I. du Pont de Nemours and Company; Wilmington, DE;									
EPX;									
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1. .1447									
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Query Match 7.0%; Score 203.4; DB 6; Length 1447;									
Best Local Similarity 61.3%; Pred. No. 6.1e-28;									
Matches 399; Conservative 0; Mismatches 186; Indels 86; Gaps 1;									
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DB	436	GTGCTATCTCCTAGATATATATATGTTGGCTTGGCATACCTGTGTATTAGCAATTTA	495						
QY	2202	TCTGTTTATAGTTGAGTTTATGATTATTTGGGTTTCACAAAGAGCTTCATGACATTAAT	2261						
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QY	2262	TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCC	2321						
DB	556	GCCTTACAAATATCTTCATGCTACCCATCACATCTACAATAAACAGAAACACTCTCTCCC	615						
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DB	616	TTTTGCTGGTTG-----	628						
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QY	2442	ATATCTCAGGCTATACCGCAGTGATAGCGCTGTTTATAGTGGCGATTCATCTCATAAAC	2501						
DB	650	ATATCTCAGGCAATTACCGCATAGCTTTGTTGTTTTTTATGCGCAATCCATTTTACTACA	709						
QY	2502	CATCTGAGTCTTTGTTTTTGGAGGAGATATGGACAGCAGCATCCATGATTGATACATAT	2561						
DB	710	CATTTGGCCCTCATATTATCATTTGAGGGGGTTTTGGACTGCAATATTCATGATTGCAATCAT	769						
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DB	770	GGAAAATTGGCCCTGTTATGGGTCGTGTTACACACCATTCATCACTACATATTCGG	829						
QY	2622	CATAACTATGGTCAATTATACCATATGGATGGACTGGATGTTTGGCTCTCTT	2672						
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LOCUS	1210 bp DNA linear PAT 20-DEC-2002								
DEFINITION	Sequence 29 from patent US 6465717.								
ACCESSION	AR237881								
VERSION	AR237881.1 GI:27282714								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 1210)								
AUTHORS	Famodu,O.O. and Rafaleki,J.A.								
TITLE	Sterol metabolism enzymes								
JOURNAL	Patent: US 6465717-A 29 15-OCT-2002;								

FEATURES		source		Location/Qualifiers	
ORIGIN					
Query Match 6.4%; Score 188; DB 6; Length 1210;					
Best Local Similarity 59.8%; Pred. No. 4.9e-25;					
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;					
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Qy	2262	TCTCTATAGCATCTCCATGCTACCCATCATATGTACAAACAGCAAAACACACTCTCTCC	2321		
Db	428	ACTATACAGCACTCATATGCAACCCACCACTTTTACACAGAGNATACCTTATCACC	487		
Qy	2322	ATTTGGCGGTATGTCAAAGCTATATGTCTCTCAATTAATTTCAAGAGCTTGTATCAATGG	2381		
Db	488	ATTTG-----CTGGACTAGCAATTCATCCATTTGGACGGG	492		
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Db	702	CACAACATGGCACTACACCGTGGATGGAGCTGGCTGTTTGGACCCCT	751		
RESULT 15					
BT009523					
LOCUS	Triticum aestivum clone wri.pk0107.a5:fls		linear		PLN 20-JUN-2003
DEFINITION	Triticum aestivum clone wri.pk0107.a5:fls, full insert mRNA sequence.				
ACCESSION	BT009523				
VERSION	BT009523.1 GI:32129074				
KEYWORDS	FLI CDNA.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.				
AUTHORS	1. (bases 1 to 1210) Tingey, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H., Caraher, N.R., Hanafey, M.K. and Hainey, C.F.				

TITLE Direct Submission  
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and  
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,  
USA

FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 6.4%; Score 188; DB 15; Length 1210;  
Best Local Similarity 59.8%; Pred. No. 4.9e-25;  
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;  
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QY 2082 GCCTTGGTACACTCTTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141  
DB 248 GCCTTCTACTGTGCTCTTCGCTCGTATCTGAGCACATGATGAGAGTGGATGGACAG 307  
QY 2142 ATGTACTCTACACTTGAACATTTCAACTGGTTCTCTGTTCTCTACATAGCTCTCTA 2201  
DB 308 GTGTTTCTTTTCATATCAGCGAAGTTGGTTGGCCTATGTACATTTATCTATGTCTCTATA 367  
QY 2202 TCTTGTGTTTAGTTGAGTTTATGATTTTATTTGGGTTTCAAGAGCTTCATGACATTAAT 2261  
DB 368 TCTCATCTTTTGGAGTTTGGAAATTTACTGGATGCAACGAGAGTTGCAATGACATAAGCC 427  
QY 2262 TCTTATAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCC 2321  
DB 428 ACTATACAGACCTTACATGCAACCCACACATTTACAAAGAGGATACCTATCACC 487  
QY 2322 ATTTGCCGATATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTTGTATCAATGG 2381  
DB 488 ATTTG----- 492  
QY 2382 TGACTTCTTTACTTGATGTTTTCGGGTTTTCAGGGCTCGCATTCCTCCGCTGGACGGG 2441  
DB 493 -----CTGGACTAGCATTCCTCCATTTGGACGGG 521  
QY 2442 ATACTTCAGGCTATACCGACGTGATAGCGCTGTTTATAGTCCGATTTCATCTCAATAACA 2501  
DB 522 ATACTGCAAGCCATATCGACGTGATGCTCTGTTCTTCTCCGATGCACTTCAGGACG 581  
QY 2502 CATCTGAGTCTTTGTTTGGAGGGGATATGGACAGCAAGCATCCATGATTGCATACAT 2561  
DB 582 CACATTGCTCTCTATTATCATAGAGCGGTGTGGACGGCAAAACATCCAGACTGCATCCAC 641  
QY 2562 GGTAACTCTGGCCTATATAGGTGAGGATACCATACCATACCATACCATACCATACCAAG 2621  
DB 642 GGCAAGATCTGGCCGGTATGGCGCGGCTACCAACCATCCACCAACCAACGACGTACCGG 701  
QY 2622 CATAACTATGGTCAATTATACCATATGATGGAGTGGATGTTGGCTCTCT 2671  
DB 702 CACACTATGGCACTACACCGTGGATGGACTGGCTGTTGGCACCCCT 751

Search completed: March 7, 2006, 13:11:49  
Job time : 14455 secs



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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 08:57:37 ; Search time 1580 Seconds  
(without alignments)  
12338.118 Million cell updates/sec

Title: US-10-736-318-22

Perfect score: 2925

Sequence: 1 gtttgattattggtgc.....tcaattggactaaatctg 2925

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2925	100.0	2925	6	ABK89916 Gene enco
2	2925	100.0	2925	12	ADQ28843 Arabidops
3	924.4	31.6	1889	6	ABK89915 Gene enco
4	924.4	31.6	1889	12	ADQ28841 Thale cre
5	464.2	15.9	1164	3	AAC41897 Arabidops
6	461	15.8	1175	6	ABK89915 Arabidops
7	347.2	11.9	846	6	ABK89915 Arabidops
8	203.4	7.0	1447	8	ABK15834 cDNA enco
9	203.4	7.0	1447	12	ADQ19006 Soybean s
10	189.4	6.5	833	12	ADQ15356 Rice isop
11	188	6.4	1335	12	ADQ15599 Wheat iso
12	188	6.4	1210	8	ABK15835 cDNA enco
13	188	6.4	1210	12	ADQ19008 Wheat ste
14	187	6.4	911	8	ABK15832 cDNA enco
15	187	6.4	911	12	ADQ19002 Maize ste
16	184.4	6.3	828	12	ADQ15677 Corn isop
17	179.6	6.1	825	12	ADK14887 Rice OGDW
18	179.6	6.1	1318	8	ABK15833 cDNA enco
19	179.6	6.1	1318	12	ADQ19004 Rice ster

20	173.8	5.9	1070	8	ABX15825	Abx15825 cDNA enco
21	173.8	5.9	1070	12	ADI18988	Adi18988 Maize ste
22	161.8	5.5	1381	5	AH50964	Ah50964 Sterol CS
23	151.8	5.2	635	12	ADI45491	Adi45491 Banana is
24	142.4	4.9	699	13	ADX4989	Adx4989 Plant ful
25	137.2	4.7	446	3	AA69689	Aa69689 Eucalyptu
26	118.4	4.0	300	10	ABX86054	Abx86054 Corn ear-
27	104.6	3.6	285	6	ABL72194	Ab172194 Corn tags
28	93.4	3.2	404	13	ADX11411	Adx11411 Plant ful
29	90.8	3.1	269	10	ABX81919	Abx81919 Corn ear-
30	90	3.1	459	8	ABX15827	Abx15827 cDNA enco
31	90	3.1	459	12	ADI18992	Adi18992 Soybean s
32	88.4	3.0	304	6	ABL70846	Ab170846 Corn tass
33	82.8	2.8	314	10	ABX88998	Abx88998 Corn ear-
34	72	2.5	1179	6	ABQ49604	Abq49604 Oligonuc1
35	72	2.5	1179	6	ABQ49605	Abq49605 Oligonuc1
36	71	2.4	495	8	ABX15828	Abx15828 cDNA enco
37	71	2.4	495	12	ADI18994	Adi18994 Wheat ste
38	70	2.4	6668	6	ABL33697	Ab133697 Human imm
39	69.4	2.4	360	8	ABX15826	Abx15826 cDNA enco
40	69.4	2.4	360	12	ADI18990	Adi18990 Rice ster
41	68.6	2.3	277	7	ADS70263	Adx70263 Corn seed
42	68.4	2.3	431	8	ABX40393	Abx40393 Bovine ES
43	68.4	2.3	6960	6	ABL34399	Ab134399 Human imm
44	68	2.3	612	14	ACL64894	Ac164894 M. xanthu
45	67.2	2.3	428	8	ABX35408	Abx35408 Bovine ES

## ALIGNMENTS

RESULT 1

ABK89916

ID ABK89916 standard; DNA; 2925 BP.

XX AC ABK89916;

XX DT 21-OCT-2002 (first entry)

XX DE Gene encoding Arabidopsis thaliana dwf7 homologue, HDP7.

XX KW Dwarf7; dwf7; plant cell; sterol composition; cholesterol; plant regulatory defect; plant growth; plant; HDP7; ds.

XX OS Arabidopsis thaliana.

XX FH Key Location/Qualifiers

FT CDS 1506..2720

FT /\*tag= a

FT /product= "HDP7"

FT exon 1506..1734

FT /\*tag= b

FT /number= 1

FT intron 1735..2023

FT /\*tag= c

FT /number= 1

FT exon 2024..2329

FT /\*tag= d

FT /number= 2

FT intron 2330..2415

FT /\*tag= e

FT /number= 2

FT exon 2416..2717

FT /\*tag= f

FT /number= 3

US2002068822-A1.

06-JUN-2002.

02-FEB-2001; 2001US-00775879.

02-FEB-2000; 2000US-0179901P.

XX (CHOE/) CHOE S.  
PA (FELD/) FELDMANN K A.  
XX PI  
XX Choe S, Feldmann KA;  
XX WPI; 2002-582494/62.  
DR P-PSDB; AAU99580.  
XX Novel isolated dwf7 polynucleotide for altering sterol composition of a  
PT plant, by introducing polynucleotide into plant cell to produce  
PT transformed plant cell and producing transgenic plant from transformed  
PT cell.  
XX  
XX Claim 7; Fig 10; 53pp; English.  
XX The present invention relates to the isolation of dwarf7 (dwf7) mutants  
CC and encoding polynucleotides that impart at least one dwf7 mutant  
CC phenotype when expressed in a plant. The polynucleotide sequences  
CC encoding the mutant dwf7 proteins are useful for producing transgenic  
CC plants from transformed plant cells. The polynucleotide sequences are  
CC useful for altering the sterol composition of a plant relative to the  
CC wild-type plant. The transgenic plant has less cholesterol or increased  
CC sterol production relative to the wild-type plant. The mutant sequences  
CC are also useful for isolating or creating other mutant cell gene alleles,  
CC and for detecting plant regulatory defects which can affect plant growth.  
CC The present sequence encodes Arabidopsis thaliana dwf7 homologue protein,  
CC HDF7  
XX  
SQ Sequence 2925 BP; 779 A; 603 C; 510 G; 1033 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2925; DB 6; Length 2925;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2925; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTTGGTATTATTTGGATGACAGAGAGCTTTCATGACATTAAGCCCTCTCTATAAGTATCT 60  
DB 1 GTTTGGTATTATTTGGATGACAGAGAGCTTTCATGACATTAAGCCCTCTCTATAAGTATCT 60  
QY 61 CCATGCCACCCATCATATCTACAAAGCAAGCAATACACTCTCTCCATTTGCCGGTAAGTG 120  
DB 61 CCATGCCACCCATCATATCTACAAAGCAAGCAATACACTCTCTCCATTTGCCGGTAAGTG 120  
QY 121 TTTTTCAGTTTGTCTTCTTGTAGTTCTTGTAAAGATTGGTACGATTTAGTTCTTATACCG 180  
DB 121 TTTTTCAGTTTGTCTTCTTGTAGTTCTTGTAAAGATTGGTACGATTTAGTTCTTATACCG 180  
QY 181 AAAAGACTTTTGTGACGAGCTGCTTGTACTCCAAATCACATTTTTCATTCCTATCCATAA 240  
DB 181 AAAAGACTTTTGTGACGAGCTGCTTGTACTCCAAATCACATTTTTCATTCCTATCCATAA 240  
QY 241 AGTAAACAGAAAGGCTAGAAATTAATAAATGTGACGTGCATTAATCTTCAATATGTCCAG 300  
DB 241 AGTAAACAGAAAGGCTAGAAATTAATAAATGTGACGTGCATTAATCTTCAATATGTCCAG 300  
QY 301 AGACTTCTGACTTAAACAGAGTTAGATCTTTTGTGTTTCTTCTGCTCGGACTGATTT 360  
DB 301 AGACTTCTGACTTAAACAGAGTTAGATCTTTTGTGTTTCTTCTGCTCGGACTGATTT 360  
QY 361 GGAATAGCAGAGAGTTCTTTTATCTACTTCCCTGGAGTGTATCTTGGTAAATCCAAAGGA 420  
DB 361 GGAATAGCAGAGAGTTCTTTTATCTACTTCCCTGGAGTGTATCTTGGTAAATCCAAAGGA 420  
QY 421 TGTGACATCTAAATATTAATCTTGTAACTTCTTACGTTTGTGTTTGTAAAGGCTTGCATTC 480  
DB 421 TGTGACATCTAAATATTAATCTTGTAACTTCTTACGTTTGTGTTTGTAAAGGCTTGCATTC 480  
QY 481 CCCAGTAGCGGATCTTAAAGCTGTACCGCATGTAGCGCTGTATAGTGCCTAAT 540  
DB 481 CCCAGTAGCGGATCTTAAAGCTGTACCGCATGTAGCGCTGTATAGTGCCTAAT 540  
QY 541 CATTTCACAACTCATATAGTCTTTTGTTCATCGAAGCGATATGAGCGCGCAATCCAT 600  
DB 541 CATTTCACAACTCATATAGTCTTTTGTTCATCGAAGCGATATGAGCGCGCAATCCAT 600

DB 541 CATTTCACAACTCATATAGGTCCTTTTGTTCATGGAAGCGATATGAGCGCGCAATCCAT 600  
QY 601 GACTGCATCCATGCGCAACATCTGCGCCAGTAATAGGGTGCAGGATACCATACGATACACCAC 660  
DB 601 GACTGCATCCATGCGCAACATCTGCGCCAGTAATAGGGTGCAGGATACCATACGATACACCAC 660  
QY 661 AGCAGATACAAGCATAAATCTATGTCATTTATACCATATGATGATGATGATGATGATGATGAT 720  
DB 661 AGCAGATACAAGCATAAATCTATGTCATTTATACCATATGATGATGATGATGATGATGATGAT 720  
QY 721 CTTAGGATCTCTCTTTAGAGAAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGTGA 780  
DB 721 CTTAGGATCTCTCTTTAGAGAAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGTGA 780  
QY 781 GAATGCCACCTTGGGTTTGTCTTCTGTTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840  
DB 781 GAATGCCACCTTGGGTTTGTCTTCTGTTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840  
QY 841 AGCCTTCTTGTGTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
DB 841 AGCCTTCTTGTGTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
QY 901 TATATGTTTACAAACATTTGCTGTAGTTTAAACATGATAAATGTTGATGATCTTTGTC 960  
DB 901 TATATGTTTACAAACATTTGCTGTAGTTTAAACATGATAAATGTTGATGATCTTTGTC 960  
QY 961 AAGACTCCATTTTGTGTTTAAAGGTAACCTTGAATCTCATAGATTTGTCGATTTGTTGATTT 1020  
DB 961 AAGACTCCATTTTGTGTTTAAAGGTAACCTTGAATCTCATAGATTTGTCGATTTGTTGATTT 1020  
QY 1021 TCCATTTTTCAGGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTAAACACC 1080  
DB 1021 TCCATTTTTCAGGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTAAACACC 1080  
QY 1081 CCAAAATTTCAAAAGATCTCAACCAATCAAAATGCTGCTGCCGCCCAATATATAGATGGGCCA 1140  
DB 1081 CCAAAATTTCAAAAGATCTCAACCAATCAAAATGCTGCTGCCGCCCAATATATAGATGGGCCA 1140  
QY 1141 GTTAATCCGCTGAGCTTTTACTCTTTAGACCTTACCTTAGACAGTTAGACACCTGCTAATTA 1200  
DB 1141 GTTAATCCGCTGAGCTTTTACTCTTTAGACCTTACCTTAGACAGTTAGACACCTGCTAATTA 1200  
QY 1201 ATGAGTTTCTTTTCTTGTTCAGCAAGTTTACTCTGTGTTTACTTGTAGAGTTGATTTAATGG 1260  
DB 1201 ATGAGTTTCTTTTCTTGTTCAGCAAGTTTACTCTGTGTTTACTTGTAGAGTTGATTTAATGG 1260  
QY 1261 TAGTAAACGCAATTTAAACCCCTTATAAGTTTAAATCGTATTTCAACGAATGACCCAGAGACTT 1320  
DB 1261 TAGTAAACGCAATTTAAACCCCTTATAAGTTTAAATCGTATTTCAACGAATGACCCAGAGACTT 1320  
QY 1321 TAAATTAATCCATCGTTAACCCCTCCACTTCAAAATTTCTTTTAAAGTAGCAATCATTT 1380  
DB 1321 TAAATTAATCCATCGTTAACCCCTCCACTTCAAAATTTCTTTTAAAGTAGCAATCATTT 1380  
QY 1381 AAATATTTGATGTTTGTCTTCAATTCGAAAATTTGTAGCTTACAGATCTCTCAAAGCTCTCTCTGTT 1440  
DB 1381 AAATATTTGATGTTTGTCTTCAATTCGAAAATTTGTAGCTTACAGATCTCTCAAAGCTCTCTCTGTT 1440  
QY 1441 GGCCTATCTCTCTCTCTAAACAAACGATAGTAAACACTTGACACAGATTTGACTTCTCGGG 1500  
DB 1441 GGCCTATCTCTCTCTCTAAACAAACGATAGTAAACACTTGACACAGATTTGACTTCTCGGG 1500  
QY 1501 GTTTCATGCGGCGGACTATGGCAGATTAATGATCAGATCTCAATGAGACTCTCTTTT 1560  
DB 1501 GTTTCATGCGGCGGACTATGGCAGATTAATGATCAGATCTCAATGAGACTCTCTTTT 1560  
QY 1561 ACAACCGAATGCTTCTGAGTCACTTTTGTCCGGTGAATCTATGCGGAACCTTTTACCAAT 1620  
DB 1561 ACAACCGAATGCTTCTGAGTCACTTTTGTCCGGTGAATCTATGCGGAACCTTTTACCAAT 1620  
QY 1621 TCCCTCAGACATGGCTCCGGAACCTACCTCCGCGGAAACATATCTCTTACTCTCTCGGCT 1680  
DB 1621 TCCCTCAGACATGGCTCCGGAACCTACCTCCGCGGAAACATATCTCTCTCTCTCGGCT 1680

1681 TCCTCTGGTCTCTACATCTATTACCTTAAACTCAACGTTTACGTCCTCCCAAGGTTACT 1740  
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1801 GCCTGATAGATTGTGTTATACGTTTAACTTTTCTTACTGTTTACTTTTCAGTTCTTGTGTC 1860  
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1981 TTAGTTCTATTTCTGCTTGGTTTCTTCTATTTTGTGGTTAGAAATCCATTCCTACGAGA 2040  
2041 AAGGCAATGCTTTTGCAAAATATACGTTGCAATGAAGGCTATGCTTTGGTACACTCTTCTT 2100  
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2521 TGGAGGGATATGGACAGCAAGCATCCATGATTGTCATACATGTTAAACATCTGCGCTATAA 2580  
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2581 TGGGTGCAGGATACCATACCATACACATACATACATACATACATACATACATACATACAT 2640  
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2641 CCATATGATGAGTGGATGTTTGGTCTCTTATGTTTCTTTAGCAGAAAAAGACAGTT 2700  
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2701 TCAAGGAGAAAGAAAGTGCAGATGTTCAATGCTACATGTTATCTTCTATATGTTGCTCT 2760  
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2761 TCTCGTGAATCTTATTAACCTTTCTTAATCACTTTGGTGAATTAACCAATGACTGCA 2820  
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2881 ATTATATTAATTTGCTGATGAAGAGTTCAAAATTTGGACTAAATCTG 2925  
2881 ATTATATTAATTTGCTGATGAAGAGTTCAAAATTTGGACTAAATCTG 2925

RESULT 2  
ADQ28843  
ID ADQ28843 standard; DNA; 2925 BP.  
XX AC ADQ28843;  
XX DT 23-SEP-2004 (first entry)  
XX Arabidopsis DWF7/STEL homologue DNA.  
XX STE1; dwarf7; dwf7; sterol; plant breeding; agricultural production;  
KW flowering; leaf production; fruit production; branching; seed production;  
KW cholesterol; brassinosteroid; sterol synthesis; DWF7/STEL; gene; ds.  
XX Arabidopsis.  
XX US2004133948-A1.  
XX PD 08-JUL-2004.  
XX PF 15-DEC-2003; 2003US-00736318.  
XX PR 02-FEB-2000; 2000US-0179901P.  
XX PR 02-FEB-2001; 2001US-00775879.  
XX (ARIZ-) ARIZONA BOARD OF REAGENTS.  
XX Choe S, Feldmann KA;  
XX WPI; 2004-517063/49.  
XX DR P-PSDB; ADQ28844.  
XX DR GENBANK; AAF32466.  
XX New isolated dwarf 7 (dwf7) polynucleotide, useful for conferring desired  
PT traits on essentially any plant and for altering sterol composition of a  
PT plant thus increasing or reducing cholesterol content.  
XX Claim 6; SEQ ID NO 22; 52pp; English.  
XX The invention relates to an isolated dwarf7 (dwf7) polynucleotide that  
CC imparts at least one dwf7 mutant phenotype when expressed in a plant. The  
CC invention also relates to a recombinant vector comprising the dwf7  
CC polynucleotide and control elements that are operably linked to the  
CC polynucleotide where a coding sequence within the polynucleotide can be  
CC transcribed and translated in a host cell, and at least one of the  
CC control elements is heterologous to the coding sequence, a host cell  
CC transformed with the recombinant vector above, a method of producing a  
CC DWF7 polypeptide, a transgenic plant comprising the polynucleotide, a  
CC method of producing a transgenic plant and a method of altering the  
CC sterol composition of a plant relative to the wild-type plant. The dwf7  
CC polynucleotides and polypeptides are useful for producing transgenic  
CC plants which display at least one dwf7 phenotype, so that the resulting  
CC plants have altered structure or morphology. The transgenic plants are  
CC useful in plant breeding, in agricultural production or in industrial  
CC applications. The dwf7 polynucleotides are useful for isolating or  
CC creating other mutant alleles and for enhancing certain features such as  
CC flowering, producing larger leaves or fruit, increased branching and  
CC increased seed production. They are also useful for conferring desired  
CC traits on any plant, for altering sterol composition of a plant thus  
CC increasing or reducing cholesterol content and for providing a tool for

CC studying the biosynthesis of brassinosteroids. The dwf7 control element  
CC is useful as a plant promoter to express any protein of interest in a  
CC transgenic plant, particularly to express a protein involved in  
CC brassinosteroid biosynthesis. The Dwf7 polypeptide is involved in any  
CC biochemical applications, e.g., regulation of sterol synthesis,  
CC modification of elongation of plant structures and experimental or  
CC industrial biochemical applications. This sequence represents DNA  
CC encoding an Arabidopsis DWf7/STB1 polypeptide homologue, used in the  
CC scope of the invention.

XX  
SQ Sequence 2925 BP; 779 A; 603 C; 510 G; 1033 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2925;	DB 12;	Length 2925;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2925;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	GTGTTGGTATTATGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT	60
DB	1	GTGTTGGTATTATGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT	60
QY	61	CGATGCCACCCATCATATCTACAAAGCAGAGATACACTCTCTCGATTTGCCGGTAAGTG	120
DB	61	CGATGCCACCCATCATATCTACAAAGCAGAGATACACTCTCTCGATTTGCCGGTAAGTG	120
QY	121	TTTTTCAGTTTGTCTCTTTAGTTCTTGTAAGAGATTGGTAGCATTTAGTTTCTTACCCAG	180
DB	121	TTTTTCAGTTTGTCTCTTTAGTTCTTGTAAGAGATTGGTAGCATTTAGTTTCTTACCCAG	180
QY	181	AAAAGAATTGTCAGCAGCTGCTTGTACTCCAAATCACATTTTGGCATTCCTTATCCATAA	240
DB	181	AAAAGAATTGTCAGCAGCTGCTTGTACTCCAAATCACATTTTGGCATTCCTTATCCATAA	240
QY	241	AGTAACAGAAAGGCTAGAAATTATATAAATGTCAGCTGCATTAATTTACATATGTCAGAG	300
DB	241	AGTAACAGAAAGGCTAGAAATTATATAAATGTCAGCTGCATTAATTTACATATGTCAGAG	300
QY	301	AGACTTCTGACTTAAACAGAGTTTAGATCTTTGTGTTTCTCTCTGCTCTCGGACTGAT	360
DB	301	AGACTTCTGACTTAAACAGAGTTTAGATCTTTGTGTTTCTCTCTGCTCTCGGACTGAT	360
QY	361	GGAAATGACAGAGAGTTCTTTATCTACTTCCCTGGAGTGTATCTTGGTTAAATCCAAAGA	420
DB	361	GGAAATGACAGAGAGTTCTTTATCTACTTCCCTGGAGTGTATCTTGGTTAAATCCAAAGA	420
QY	421	TGTGACATCTAAATATATCTGTAACTTCTCTACGTTTGTGTTTACAGGCTTGCATTC	480
DB	421	TGTGACATCTAAATATATCTGTGTAACTTCTCTACGTTTGTGTTTACAGGCTTGCATTC	480
QY	481	CCGAGTAGCGGATTAAGGCTGTACCGCATGTGATAGCGCTGTATAGTGCCAAAT	540
DB	481	CCGAGTAGCGGATTAAGGCTGTACCGCATGTGATAGCGCTGTATAGTGCCAAAT	540
QY	541	CATTTCACAACTCATATAGTCTTTTGTTCATCGAAGCGATATGGAACGCAATCCAT	600
DB	541	CATTTCACAACTCATATAGTCTTTTGTTCATCGAAGCGATATGGAACGCAATCCAT	600
QY	601	GACTGCATCCATGGCAACATCTGGCAGTAATGGGTGCAGGATACCATAGATACACCC	660
DB	601	GACTGCATCCATGGCAACATCTGGCAGTAATGGGTGCAGGATACCATAGATACACCC	660
QY	661	ACGACATACAGCATTAATGTCATTATACCATATGGATGGATTTGGTCTCT	720
DB	661	ACGACATACAGCATTAATGTCATTATACCATATGGATGGATTTGGTCTCT	720
QY	721	CTTAGGGATCCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGTGA	780
DB	721	CTTAGGGATCCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGTGA	780
QY	781	GAATGCCACCTCTGCTTCT	840
DB	781	GAATGCCACCTCTGCTTCT	840
QY	841	AGGCTTTCTGTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	900

DB	841	AGGCTTTCTGTTCTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT	900
QY	901	TATATTTGTACAAACATTTGCTGTCTAGTTTAAACATGTAATGTTTGCATGATCTTTGC	960
DB	901	TATATTTGTACAAACATTTGCTGTCTAGTTTAAACATGTAATGTTTGCATGATCTTTGC	960
QY	961	AAGACTCCAAATTTTGTGTTTAAAGTAAACCTTGAATCTCATAGATTGTCGATTGTTGTA	1020
DB	961	AAGACTCCAAATTTTGTGTTTAAAGTAAACCTTGAATCTCATAGATTGTCGATTGTTGTA	1020
QY	1021	TCCATTTTCAGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTAAACACC	1080
DB	1021	TCCATTTTCAGTACGGTTCTGTAGACTGTAGTCTTGTGTGACAGCTCCGGCTTAAACACC	1080
QY	1081	CCAAATTTCAAAGATCTCACCAATCAAAATGCTGGCTGGCCCAATATATAGATGGGCCA	1140
DB	1081	CCAAATTTCAAAGATCTCACCAATCAAAATGCTGGCTGGCCCAATATATAGATGGGCCA	1140
QY	1141	GTTAATCCGTCAGCTTTTACTCTTTTAGACCTTACTTTAGACAGTTAGACACCTGCTTA	1200
DB	1141	GTTAATCCGTCAGCTTTTACTCTTTTAGACCTTACTTTAGACAGTTAGACACCTGCTTA	1200
QY	1201	ATGAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	1260
DB	1201	ATGAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	1260
QY	1261	TAGTAAACGCAATTTTAAACCTTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT	1320
DB	1261	TAGTAAACGCAATTTTAAACCTTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT	1320
QY	1321	TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1380
DB	1321	TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1380
QY	1381	AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1440
DB	1381	AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1440
QY	1441	GCCCATATCT	1500
DB	1441	GCCCATATCT	1500
QY	1501	GTTTCATGCGCGGACTATGCGAGATTAATATGATCAGATCGTCAATGAGACCTCTTTT	1560
DB	1501	GTTTCATGCGCGGACTATGCGAGATTAATATGATCAGATCGTCAATGAGACCTCTTTT	1560
QY	1561	ACAAACGGAATGTTCTGAGTCACTTTTGGCGGTGAACTCTATGGGAACTTTTACCAAT	1620
DB	1561	ACAAACGGAATGTTCTGAGTCACTTTTGGCGGTGAACTCTATGGGAACTTTTACCAAT	1620
QY	1621	TCTCTCAGACATGGCTCCGGAACTACCTCCCGGAAACATATCTACTTCTCTCTCTCTCT	1680
DB	1621	TCTCTCAGACATGGCTCCGGAACTACCTCCCGGAAACATATCTACTTCTCTCTCTCTCT	1680
QY	1681	TCTCTGTTGTTCTTACATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1740
DB	1681	TCTCTGTTGTTCTTACATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1740
QY	1741	TTTTTCAATTTTCGATGTTCTGTTTGTGAAACCTTTCTTTTGTGATTCCTTCGATTGTA	1800
DB	1741	TTTTTCAATTTTCGATGTTCTGTTTGTGAAACCTTTCTTTTGTGATTCCTTCGATTGTA	1800
QY	1801	GCTCATAGATTGTTGTTATACGTTTAACTTTTCTTACTTCTTACTTCTTACTTCTTCT	1860
DB	1801	GCTCATAGATTGTTGTTATACGTTTAACTTTTCTTACTTCTTACTTCTTACTTCTTCT	1860
QY	1861	TTCTACTTCTCAATTTAAATTTAGTTTAAAGTTTAAATTTTGGCTTAAATCCACATTTT	1920
DB	1861	TTCTACTTCTCAATTTAAATTTAGTTTAAAGTTTAAATTTTGGCTTAAATCCACATTTT	1920
QY	1921	AGTTGAAATCTTCCATGAAATTTGAGCTCAAAATATACCAATGAAATTTGAGTTTCT	1980



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QY 61 CCATGCCACCCATCATATCTACAAACAGCAGATACACTCTCTCCATTTGCCGTAAGTG 120
DB 989 CCATGCCACCCATCATATCTACAAACAGCAGATACACTCTCTCCATTTGCCGTAAGTG 1048
QY 121 TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAGATTTGGTAGCATTTAGTTTCTTACCCAG 180
DB 1049 TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAGATTTGGTAGCATTTAGTTTCTTACCCAG 1108
QY 181 AAAAGACTTTGTGACAGAGCTGCTGTACTTCCAAATCACAATTTTGCATTCCTTATCCATAA 240
DB 1109 AAAAGACTTTGTGACAGAGCTGCTGTACTTCCAAATCACAATTTTGCATTCCTTATCCATAA 1168
QY 241 AGTAACAGAAAGGCTAGAAATATATAAATGTCAGCTGCATTAATCTTACATATGTCAGAG 300
DB 1169 AGTAACAGAAAGGCTAGAAATATATAAATGTCAGCTGCATTAATCTTACATATGTCAGAG 1228
QY 301 AGACTTCTGACTTAACACAGATTTAGATCTTTTGTCTTCTCTTCTGCTCTCGGACTGATT 360
DB 1229 AGACTTCTGACTTAACACAGATTTAGATCTTTTGTCTTCTCTTCTGCTCTCGGACTGATT 1288
QY 361 GGAATGACGAGAAAGTTCTTTATCTACTTCCCTCGAGTGTATCTTGGTTAATCCAAAGA 420
DB 1289 GGAATGACGAGAAAGTTCTTTATCTACTTCCCTCGAGTGTATCTTGGTTAATCCAAAGA 1348
QY 421 TGTGACATCTAAATATTTACTTGTAACTTCTTACGTTTTTGTGTACAGGCTTGCA-TTC 479
DB 1349 TGTGACATCT-AAATATCTTGTAACTTCTTACGTTTTTGTGTACAGGCTTGCAATTC 1407
QY 480 ACCCAGTAGACGGGATCTTAAAGGCTGTACCGCATGTGATAGCGCTG-TTATAGTGCCAA 538
DB 1408 ACCCAGTAGACGGGATCTTAAAGGCTGTACCGCATGTGATAGCGCTGTTTATAGTGCCAA 1467
QY 539 TTCATTTCACATCTCATATAGTCTTTTGTTCATGGAAGCGCATATGAGCGCGAAATCC 598
DB 1468 TTCATTTCACATCTCATATAGTCTTTTGTTCATGGAAGCGCATATGAGCGCGAAATCC 1527
QY 599 ATGACTGCATCCATGGCAACATCTGCCAGTATGGTGGCGAGATACCATACATACACC 658
DB 1528 ATGACTGCATCCATGGCAACATCTGCCAGTATGGTGGCGAGATACCATACATACACC 1587
QY 659 ACACGACATACAAAGCATAACTATGGTCATTATATACCATATGGATGGATTTGGGCT 718
DB 1588 ACACGACATACAAAGCATAACTATGGTCATTATATACCATATGGATGGATTTGGGCT 1647
QY 719 CTCTTAGGGATCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGT 778
DB 1648 CTCTTAGGGATCTCTCTTAGAAGAGATGACAAAGACAGCTTCAAGAAAGCAGAGT 1707
QY 779 GAGAATGCCACATTTGGTTTGTCTTCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGT 838
DB 1708 GAGAATGCCACATTTGGTTTGTCTTCTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGT 1767
QY 839 TCAGCCTTTCTTGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 898
DB 1768 TCAGCCTTTCTTGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1827
QY 899 ATTATATTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTTTGTGATGATCTTT 958
DB 1828 ATTATATTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTTTGTGATGATCTTT 1887
QY 959 GC 960
DB 1888 GC 1889
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RESULT 4

ID ADQ28841 standard; DNA; 1889 BP.

XX AC ADQ28841;

XX 23-SEP-2004 (first entry)

```
XX Thale cress dwarf7 (dwf7) DNA.
DE Thale cress; dwarf7; dwf7; sterol; plant breeding;
XX agricultural production; flowering; leaf production; fruit production;
KW branching; seed production; cholesterol; brassinosteroid;
KW sterol synthesis; gene; ds.
XX Arabidopsis thaliana.
OS US2004133948-A1.
XX 08-JUL-2004.
XX 15-DEC-2003; 2003US-00736318.
XX 02-FEB-2000; 2000US-0179901P.
XX 02-FEB-2001; 2001US-00775879.
XX (ARIZ-) ARIZONA BOARD OF REGENTS.
XX Choe S, Feldmann KA;
XX WPI; 2004-517063/49.
XX P-PSDB; ADQ28842.
XX New isolated dwarf 7 (dwf7) polynucleotide, useful for conferring desired
XX traits on essentially any plant and for altering sterol composition of a
XX plant thus increasing or reducing cholesterol content.
XX Claim 1; SEQ ID NO 20; 52pp; English.
XX The invention relates to an isolated dwarf7 (dwf7) polynucleotide that
XX imparts at least one dwf7 mutant phenotype when expressed in a plant. The
XX invention also relates to a recombinant vector comprising the dwf7
XX polynucleotide and control elements that are operably linked to the
XX polynucleotide where a coding sequence within the polynucleotide can be
XX transcribed and translated in a host cell, and at least one of the
XX control elements is heterologous to the coding sequence, a host cell
XX transformed with the recombinant vector above, a method of producing a
XX DWf7 polypeptide, a transgenic plant comprising the polynucleotide, a
XX method of producing a transgenic plant and a method of altering the
XX sterol composition of a plant relative to the wild-type plant. The dwf7
XX polynucleotides and polypeptides are useful for producing transgenic
XX plants which display at least one dwf7 phenotype, so that the resulting
XX plants have altered structure or morphology. The transgenic plants are
XX useful in plant breeding, in agricultural production or in industrial
XX applications. The dwf7 polynucleotides are useful for isolating or
XX creating other mutant alleles and for enhancing certain features such as
XX flowering, producing larger leaves or fruit, increased branching and
XX increased seed production. They are also useful for conferring desired
XX traits on any plant, for altering sterol content and for providing a tool for
XX increasing or reducing cholesterol content of brassinosteroids. The dwf7 control element
XX is useful as a plant promoter to express a protein of interest in a
XX transgenic plant, particularly to express a protein involved in
XX brassinosteroid biosynthesis. The DWf7 polypeptide is useful in any
XX biochemical applications, e.g., regulation of sterol synthesis,
XX modification of elongation of plant structures and experimental or
XX industrial biochemical applications. This sequence represents thale cress
XX dwarf7 (dwf7) DNA, used in the scope of the invention.
XX Sequence 1889 BP; 466 A; 385 C; 352 G; 686 T; 0 U; 0 Other;
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Query Match 31.6%; Score 924.4; DB 12; Length 1889;  
Best Local Similarity 99.6%; Pred. No. 5.8e-206;  
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
QY 1 GTTTGGTATTATTGGATGCACAGAGCTTTCATGACATTAAAGCCCTCTCTATAAGTATCT 60
DB 929 GTTTGGTATTATTGGATGCACAGAGCTTTCATGACATTAAAGCCCTCTCTATAAGTATCT 988
QY 61 CCATGCCACCCATCATATCTACAAACAGCAGATACACTCTCTTCCATTTGCCGTAAGTG 120
```





PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.	QY	462	TTTACAGGGCTTGCA-TTCACCCAGTAGACGGGATACTTTAAGGCTGTACCGCATGTGATA	520
PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.	DB	672	TTTGGCGGGCTTGCACTTTCCACCCAGTAGACGGGATACTTTAAGGCTGTACCGCATGTGATA	731
PR	24-JUN-1999;	99US-0140355P.	PR	07-SEP-1999;	99US-0152363P.	QY	521	GGCGTG-TTATAGTGCCAATTCATTTCACAACTCATATAGGCTCTTTTGTTCATGGAGCG	579
PR	28-JUN-1999;	99US-0140356P.	PR	10-SEP-1999;	99US-0153070P.	DB	732	GGCGTGTTTATAGTGCCAATTCATTTCACAACTCATATAGGCTCTTTTGTTCATGGAGCG	791
PR	29-JUN-1999;	99US-0140357P.	PR	13-SEP-1999;	99US-0153758P.	QY	580	ATATGGACGGCGAACAATCCATGCACTGCATCCATGGCAACATCTGGCAGTAATGGGTGCA	639
PR	30-JUN-1999;	99US-0140358P.	PR	15-SEP-1999;	99US-0154018P.	DB	792	ATATGGACGGCGAACAATCCATGCACTGCATCCATGGCAACATCTGGCAGTAATGGGTGCA	851
PR	01-JUL-1999;	99US-0141287P.	PR	16-SEP-1999;	99US-0154039P.	QY	640	GGATACCATACGATACACCAACAGGACATACAGCATACATATGGTCACTATATACCATATGG	699
PR	01-JUL-1999;	99US-0141842P.	PR	20-SEP-1999;	99US-0154779P.	DB	852	GGATACCATACGATACACCAACAGGACATACAGCATACATATGGTCACTATATACCATATGG	911
PR	02-JUL-1999;	99US-0142154P.	PR	22-SEP-1999;	99US-0155139P.	QY	700	ATGGATTGGATGTTTGGCTCTCTTAGGGATCTCTCTTAGAGAGATGCAACAAGAC	759
PR	02-JUL-1999;	99US-0142555P.	PR	23-SEP-1999;	99US-0155139P.	DB	912	ATGGATTGGATGTTTGGCTCTCTTAGGGATCTCTCTTAGAGAGATGCAACAAGAC	971
PR	06-JUL-1999;	99US-0142590P.	PR	24-SEP-1999;	99US-0155486P.	QY	760	AGCTTCAAGAAAGACAGAGTGAGATGCCCACTTTGGGTTTTTGTCTTCTTCTTGTCTTGT	819
PR	08-JUL-1999;	99US-0142803P.	PR	28-SEP-1999;	99US-0156559P.				
PR	09-JUL-1999;	99US-0142920P.	PR	29-SEP-1999;	99US-0156458P.				
PR	12-JUL-1999;	99US-0142977P.	PR	05-OCT-1999;	99US-0157117P.				
PR	13-JUL-1999;	99US-0143542P.	PR	06-OCT-1999;	99US-0157533P.				
PR	14-JUL-1999;	99US-0143624P.	PR	06-OCT-1999;	99US-0157865P.				
PR	15-JUL-1999;	99US-0144005P.	PR	07-OCT-1999;	99US-0158029P.				
PR	16-JUL-1999;	99US-0144085P.	PR	08-OCT-1999;	99US-0158232P.				
PR	16-JUL-1999;	99US-0144086P.	PR	12-OCT-1999;	99US-0158369P.				
PR	19-JUL-1999;	99US-0144325P.	PR	13-OCT-1999;	99US-0159293P.				
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159294P.				
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.				
PR	19-JUL-1999;	99US-0144333P.	PR	14-OCT-1999;	99US-0159329P.				
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159330P.				
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159331P.				
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159637P.				
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159638P.				
PR	20-JUL-1999;	99US-0144884P.	PR	18-OCT-1999;	99US-0159584P.				
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160741P.				
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160767P.				
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160768P.				
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160770P.				
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160814P.				
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160815P.				
PR	22-JUL-1999;	99US-0145192P.	PR	22-OCT-1999;	99US-0160980P.				
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.				
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.				
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.				
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.				
PR	27-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161405P.				
PR	27-JUL-1999;	99US-0145313P.	PR	25-OCT-1999;	99US-0161408P.				
PR	27-JUL-1999;	99US-0145918P.	PR	26-OCT-1999;	99US-0161359P.				
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161360P.				
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161361P.				
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161920P.				
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161992P.				
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161993P.				
PR	03-AUG-1999;	99US-0147038P.	PR	29-OCT-1999;	99US-0162142P.				
PR	04-AUG-1999;	99US-0147204P.							
PR	04-AUG-1999;	99US-0147302P.							
PR	05-AUG-1999;	99US-0147192P.							
PR	05-AUG-1999;	99US-0147260P.							
PR	06-AUG-1999;	99US-0147303P.							
PR	06-AUG-1999;	99US-0147416P.							
PR	09-AUG-1999;	99US-0147493P.							
PR	09-AUG-1999;	99US-0147935P.							
PR	10-AUG-1999;	99US-0148171P.							
PR	11-AUG-1999;	99US-0148319P.							
PR	12-AUG-1999;	99US-0148341P.							
PR	13-AUG-1999;	99US-0148565P.							
PR	13-AUG-1999;	99US-0148684P.							
PR	16-AUG-1999;	99US-0149368P.							
PR	17-AUG-1999;	99US-0149175P.							
PR	18-AUG-1999;	99US-0149426P.							
PR	20-AUG-1999;	99US-0149722P.							
PR	20-AUG-1999;	99US-0149723P.							
PR	20-AUG-1999;	99US-0149929P.							
PR	23-AUG-1999;	99US-0149902P.							
PR	23-AUG-1999;	99US-0149930P.							
PR	25-AUG-1999;	99US-0150566P.							
PR	26-AUG-1999;	99US-0150884P.							
PR	27-AUG-1999;	99US-0151066P.							
PR	27-AUG-1999;	99US-0151066P.							
PR	30-AUG-1999;	99US-0151080P.							
PR	30-AUG-1999;	99US-0151303P.							





Db 376 GCGGTGGTACTCTTTACTCCAACTGTTTCGGAGTACCTGGTAGAAACCTGGCTGGCAAA 435  
 QY 2142 ATGTTACTCTACACTTTGACCAATTTCAACTGGTTCCTCTGTTCTCTACATAGCTCTCTA 2201  
 Db 436 GTGCTATCTAGATTATATAATGTTGGTTGGCTTGCAATACCTTGTTGTAATTGACAAATTA 495  
 QY 2202 TCTGTTTATGTTGATTGATTTATGTTTATGTTGTTCAAAAGAGCTTCATGACATTAATTT 2261  
 Db 496 TCTAATTTATGTTAGATTGTTGTTATTTATGTTGTTCAAGAGCTTCAGGACATATAAAC 555  
 QY 2262 TCTCTATAAGCTCTCCATGCTACCCATCATATGTTACAAAGCAACCAACACACTCTCTCC 2321  
 Db 556 GCTTTTACAATATCTTCATGCTACCCATCATATGTTTACAAATTAACAGAACACTCTCTCCC 615  
 QY 2322 ATTTCGGGTATGTTCAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381  
 Db 616 TTTTGTGTTG----- 628  
 QY 2382 TGACTTCTTTACTTGTGATGTTTTCGGGTTTTCAGGCTCGCATTCATCGCTGGACGG 2441  
 Db 629 -----GCATTTCAACCCTCTTGATGG 649  
 QY 2442 ATACTTCAGCTATACCGCAGTGTAGCGCTGTTTATAGTCCGATTTCTCTCTATAACA 2501  
 Db 650 ATACTTCAGGCAATACCGCATAGCTTGTGTTGTTTATGCTCAATTCATTTACTACA 709  
 QY 2502 CATCTGAGTCTTTGTTTGGAAAGGATATGACAGCAAGCATCCATGATTGCATACAT 2561  
 Db 710 CATTTGGCCCTCATATTCATTGAGGCGTTTGGACTGCAATATTCAATGATGCAATTCAT 769  
 QY 2562 GGTAAACATCTGGCTTAATGTTGTCAGGATACCATACCATACACATACATCAACAA 2621  
 Db 770 GGAATAATTTGGCTGTTATGGTGTGCTGTTACCAACCATTCATCACAACATCATATCGG 829  
 QY 2622 CATTAATAGTTCATTTACCATATGATGATGGAGTGGATGTTGGCTCTCTT 2672  
 Db 830 CACAACACTACGGCCACTACACCATATGATGGATGGATGTTGGAACTCTT 880

## RESULT 9

AD119006  
 ID AD119006 standard; cDNA; 1447 BP.

XX AC AD119006;

XX 15-APR-2004 (first entry)

XX Soybean sterol-C5-desaturase cDNA #2.

XX Transcription factor; genetic mapping; plant breeding;

KW sterol-C5-desaturase; soybean; gene; ss.

XX Glycine max.

XX Key Location/Qualifiers

FT CDS 107..916

FT /\*tag= a

FT /product= "Sterol-C5-desaturase"

FT /partial

FT /note= "No start codon"

XX US2003229914-A1.

XX 11-DEC-2003.

XX 21-AUG-2002; 2002US-00224880.

XX 20-NOV-1998; 98US-0109283P.

PR 19-NOV-1999; 99US-00443041.

XX (FAMO/) FAMODU O O.

PA (OROZ/) OROZCO E M.

PA (RAFA/) RAFALSKI J A.

PA (SHEN/) SHEN J B.

XX Famodu OO, Orozco EM, Rafalski JA, Shen JB;

XX WPI; 2004-052051/05.

DR P-PSDB; AD119007.

XX New polynucleotide encoding a transcription factor polypeptide, useful in genetic mapping for plant breeding.

XX Claim 2; SEQ ID NO 27; 43pp; English.

XX The invention relates to a polynucleotide which encodes a transcription factor. The nucleic acid fragment is useful in genetic mapping for plant breeding. The present sequence is sterol-C5-desaturase cDNA.

XX Sequence 1447 BP; 444 A; 283 C; 294 G; 426 T; 0 U; 0 Other;

XX Query Match 7.0%; Score 203.4; DB 12; Length 1447;

XX Best Local Similarity 61.3%; Pred. No. 3.4e-37;

XX Matches 399; Conservative 0; Mismatches 166; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCCTACGAGAAAGCCATGCTTTTGCNAATATAGTGGCAATGAGGCTAT 2081

Db 316 AGATGCTATTCCTCTCAAAAGAGCCATGCTCTGCAAAATATCTGTTGCTATGAAAGCCAT 375

QY 2082 GCCTGGGTACACTCTTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141

Db 376 GCGGTGTTACTTCTTACTTCCAACTGTTTGGAGTACCTGGTAGAACTGGCTGGACAAA 435

QY 2142 ATGTACTCTACACTTGACCATTTCAACTGGTTCCTCTCTCTCTACATAGCTCTCTA 2201

Db 436 GTGCTATCTCATATTATATAATGTTGGTTGGCTTGCAATACCTTGTGTATTTAGCAATTTA 495

QY 2202 TCTGTTTATGTTGATTTATGATTTATGGGTTCAAAAGAGCTTCATGACATTAATTT 2261

Db 496 TCTAATTTATGTTAGAGTTTGGTATTTATTTGGATGTCACAGAGCTGTCAGACATAAAACC 555

QY 2262 TCTCTATAAGCATCTCCATGCTACCATCATATGATACAAAGCAAGCAACACACTCTCTCC 2321

Db 556 GCTTTTACAATATCTTCTGCTACCATCCATCATCTACAATAACAGAACACTCTCTCCCC 615

QY 2322 ATTTCCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381

Db 616 TTTTGTGTTG----- 628

QY 2382 TGACTTCTTACTTGATGTTTTCGGGTTTTCAGGCTCGCATTCATCGCTGGACGG 2441

Db 629 -----GCATTTCAACCCTCTTGATGG 649

QY 2442 ATACTTCAGGCTATACCGCAGCTGATAGCGCTGTTTATAGTCCGATTCATCTCATAACA 2501

Db 650 ATACTTCAGGCAATACCGCATAGCTTGTGTTGTTTATGCAATTCATTTACTACA 709

QY 2502 CATCTGAGTCTTTGTTTGGAAAGGATATGACAGCAAGCATCCATGATGTCATACAT 2561

Db 710 CATTTGGCCCTCATATTTCATTGAGGCGTTTGGACTGCAAAATATTTCATGATTGCAATTCAT 769

QY 2562 GGTAAACATCTGGCTTAATGTTGTCAGGATACCATACCATACACATACATCAACAA 2621

Db 770 GGAATAATTTGGCTGTTATGGTGTGCTGTTACCAACCATTCATCACAACATCATATCGG 829

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Db 830 CACAACACTACGGCCACTACCAATATGATGGATGTTGGAACTCTT 880

RESULT 10

AD145356

ID AD145356 standard; cDNA; 833 BP.

XX AD145356;

XX AD145356;



dimethylallyl alcohol; DWAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phyloquinone; mevalonate pathway; phytoesterol; brassinosteroid; ubiquinone; monoterpene; sesquiterpene; protein prenylation; chlorophyll; haeme; yield.

Triticum aestivum.

US2004010815-A1.

15-JAN-2004.

26-SEP-2002; 2002US-00259194.

26-SEP-2001; 2001US-0325277P.

04-APR-2002; 2002US-0370620P.

04-APR-2002; 2002US-0370743P.

(LANG/) LANGE B M.

(GHAS/) GHASSEMIAN M.

(BRIG/) BRIGGS S P.

(COOP/) COOPER B.

(GLAZ/) GLAZEBROOK J.

(GOLF/) GOLF S A.

(KATA/) KATAGIRI F.

(KREP/) KREPS J.

(MOUG/) MOUGHAMER T.

(PROV/) PROVART N.

(RICK/) RICKS D.

(ZHUT/) ZHU T.

Lange BM, Ghassenian M, Briggs SP, Cooper B, Glazebrook J; Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D; Zhu T;

WPI; 2004-090562/09.

New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.

Disclosure; SEQ ID NO 530; 117pp; English.

The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression cassette comprising the polynucleotide, a host cell comprising the expression cassette, and a transgenic plant comprising the expression cassette. The polypeptides and polynucleotides include those associated with the biosynthesis of isopentenyl diphosphate (IPP) and dimethylallyl alcohol (DWAPP), the biosynthesis of short-chain plastid prenyltransferases, the biosynthesis of gibberellins, the biosynthesis of carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phyloquinone biosynthesis, the mevalonate pathway, phytoesterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of monoterpenes and sesquiterpenes, protein prenylation, and biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polynucleotides. The polynucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The nucleic acid molecules are useful for targeted gene disruption, as well as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html?DocID=20040010815](http://seqdata.uspto.gov/sequence.html?DocID=20040010815). The present sequence is a Wheat isoprenoid biosynthesis-associated cDNA of the invention.

XX Sequence 1135 BP; 243 A; 292 C; 296 G; 304 T; 0 U; 0 Other;  
SQ Query Match 6.4%; Score 188; DB 12; Length 1135;  
Best Local Similarity 59.8%; Pred. No. 1.2e-33;  
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;  
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DB 220 AGATGCTGCTCCCTACAGTAGAGCTATGAAGAAGCAATAATTTGTCATCAAGGCTAT 279  
QY 2082 GCCTTGGTACACTCTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGTTGGACCA 2141  
DB 280 GCCTTTTCTACTGTGCTCTTCCGTATCTGAGCAGATGATTGAGAGTGGACACG 339  
QY 2142 ATGTTTACTCTACACTTGTGACCAATTTCAACTGGTTCCTCTGTTTCTCTCTCATATAGCTCTCTA 2201  
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QY 2202 TCTTGTTTTAGTTGAGTTTATGATTTATTTGGGTTCAAAAGAGCTTTCATGACATTAAT 2261  
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QY 2262 TCTCTATAAGCATCTCCATGCTTACCCATCATATGTACAAAGCAAAACACACTCTCTCC 2321  
DB 460 ACTATACAAGCACCTTACATGCAACCCACCACATTTTACAACAAGGAGAATACCCCTATCACC 519  
QY 2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381  
DB 520 ATTTG----- 524  
QY 2382 TGACTTCTTTACTTGATGTTTTTCGGGTTTTTCAGGGCTCGCATTCATCCGTGGACGG 2441  
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DB 554 ATACTGCAAGCCATATCGACGTGATTTGCTCTGTTCTTCTCCGATGCACTTCAGGACG 613  
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QY 2622 CATAACTATGTCATATACCATATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2671  
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XX  
AC ABX15835;  
XX  
DT 31-MAR-2003 (first entry)  
XX  
DE cDNA encoding wheat sterol C5 desaturase protein #2.  
XX  
KW Corn; wheat; rice; soybean; plant; gene; ss; sterol metabolism;  
KW sterol delta 7; reductase; sterol C5 desaturase.  
XX  
OS Triticum aestivum.  
XX  
FN US6465717-B1.  
XX  
PD 15-OCT-2002.  
XX  
PF 19-NOV-1999; 99US-00443041.  
XX



PR 20-NOV-1998; 98US-0109283P.  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Famodu OO, Rafalski JA;  
PI WPI; 2003-147075/14.  
DR P-PSDB; ABG73991.  
XX Novel polynucleotide encoding sterol metabolism enzyme useful for  
PT producing transgenic plant, has nucleotide sequence encoding the  
PT polypeptide having sterol delta-7 reductase activity.  
XX Disclosure; Col 59-62; 39pp; English.  
XX This invention relates to novel isolated polynucleotide encoding sterol  
CC metabolism enzyme. The nucleotide sequence of the invention is useful for  
CC transforming a cell by introducing the sequence into a cell. The  
CC sequences may also be useful for producing a transgenic plant, by  
CC transforming a plant cell with the cDNA sequence and regenerating a  
CC transgenic plant from the transformed plant cell. The nucleotide sequence  
CC is useful for obtaining a nucleic acid fragment encoding all or a  
CC substantial portion of the amino acid sequence encoding a sterol delta-7  
CC reductase or a sterol-C5 desaturase polypeptide. Probes derived from the  
CC nucleotide sequence of the invention may be useful for physical mapping.  
CC The present sequence represents a cDNA sequence encoding a sterol  
CC metabolism enzyme of the invention  
XX  
SQ Sequence 1210 BP; 323 A; 288 C; 293 G; 305 T; 0 U; 1 Other;  
Query Match 6.4%; Score 188; DB 8; Length 1210;  
Best Local Similarity 59.8%; Pred. No. 1.3e-33;  
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;  
QY 2022 AGAATCCATCTCCACGAGAAAGCAATGCTTTTGCMAATATACGTGGCAATGAAGGCTAT 2081  
DB 188 AGATGCTGTCCTACAGTAGAGCTATGAAGAGCAATAATTTGTCATCAAGGCTAT 247  
QY 2082 GCCTTGGTACACTCTCTCCAGCTGTCTGAGTATATGTCAGCATGGTTGGACCAA 2141  
DB 248 GCCTTTCTACTGTCTCTTCGTCGATCTGAGCAGCATGATTGAGAGTGGATGGACAG 307  
QY 2142 ATGTTACTACTACACTTGACCATTTCAACTGGTTCTCTCTCTCTACATAGCTCTCTA 2201  
DB 308 GTGTTTCTTATATCAGCGAGTGGTGGCCATGTATGATATCTATGTCCTCTATA 367  
QY 2202 TCTTGTGTTAGTTGAGTTATGATTTATTGGGTTCAAGAGCTTCATGACATTAATTT 2261  
DB 368 TCTCATCTTTGGAGTTCGGAATTTACTGGATGTCACAGAGTTCGATGACATAAAGCC 427  
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DB 428 ACTATACAGCACCCTACATGCAACCCACCACTTTTACAAACAGGAGTAACCTATCACC 487  
QY 2322 ATTTGCGGATGTGCAAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATG 2381  
DB 488 ATTTG----- 492  
QY 2382 TGACTTCTTTAATTGATGTTTTTCGGGTTTTCAGGCTCGCATTCATCGCTGGACGG 2441  
DB 493 -----CTGGACTAGCATTTCCATTCGACGG 521  
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QY 2502 CATCTGAGTCTTTTGTGTTTGGAGGATGATGACAGCAGCATCCATGATTGCATACAT 2561  
DB 582 CACATTTGCTCTCTATTCATAGAGGGGTGTGACGGCAACATCCAGACTGCATCCAC 641  
QY 2562 GGTAAACATCTGGCCTATAATGGGTGAGGATACCATACCATACCAATCAACATCAAG 2621  
DB 642 GCGAAGATCTGGCGGTGATGGCGCGGCTACCAACCATCCACACAGAGTACCGG 701

QY 2622 CATAACTATGGTCATTATACCATATGGATGGACTGGATGTTGGCTCTCT 2671  
DB 702 CACAACATATGCCACTACACCGTGGATGGACTGGCTGTTGGACCCCT 751  
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XX  
AC AD119008;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Wheat sterol-C5-desaturase cDNA #2.  
XX  
KW Transcription factor; genetic mapping; plant breeding;  
KW sterol-C5-desaturase; wheat; gene; ss.  
XX  
OS Triticum aestivum.  
XX  
FH Key Location/Qualifiers  
FT CDS 54..761  
FT /tag= a  
FT /product= "Sterol-C5-desaturase"  
FT /partial  
FT /note= "No start and stop codon"  
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PN US2003229914-A1.  
XX  
PD 11-DEC-2003.  
XX  
PF 21-AUG-2002; 2002US-00224880.  
XX  
PR 20-NOV-1998; 98US-0109283P.  
PR 19-NOV-1999; 99US-00443041.  
XX  
PA (FAMO/) FAMODU O O.  
PA (OROZ/) OROZCO E M.  
PA (RAFA/) RAFALSKI J A.  
PA (SHEN/) SHEN J B.  
XX  
PI Famodu OO, Orozco EM, Rafalski JA, Shen JB;  
XX  
XX WPI; 2004-052051/05.  
DR P-PSDB; AD119009.  
XX  
PT New polynucleotide encoding a transcription factor polypeptide, useful in  
PT genetic mapping for plant breeding.  
XX  
PS Claim 2; SEQ ID NO 29; 43pp; English.  
XX  
CC The invention relates to a polynucleotide which encodes a transcription  
CC factor. The nucleic acid fragment is useful in genetic mapping for plant  
CC breeding. The present sequence is sterol-C5-desaturase cDNA.  
XX  
SQ Sequence 1210 BP; 323 A; 288 C; 293 G; 305 T; 0 U; 1 Other;  
Query Match 6.4%; Score 188; DB 12; Length 1210;  
Best Local Similarity 59.8%; Pred. No. 1.3e-33;  
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;  
QY 2022 AGAATCCATCTCCACGAGAAAGCAATGCTTTTGCMAATATACGTGGCAATGAAGGCTAT 2081  
DB 188 AGATGCTGTCCTACAGTAGAGCTATGAAGAGCAATAATTTGTCATCAAGGCTAT 247  
QY 2082 GCCTTGGTACACTCTCTCCAGCTGTCTGAGTATATGTCAGCATGGTTGGACCAA 2141  
DB 248 GCCTTTCTACTGTCTCTTCGTCGATCTGAGCAGCATGATTGAGAGTGGATGGACAG 307  
QY 2142 ATGTTACTACTACACTTGACCATTTCAACTGGTTCTCTCTCTCTACATAGCTCTCTA 2201  
DB 308 GTGTTTCTTATATCAGCGAGTGGTGGCCATGTATGATATCTATGTCCTCTATA 367



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XX OS Zea mays.
XX PH Key Location/Qualifiers
XX FT CDS 74..646
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XX FT /product= "Sterol-C5-desaturase"
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XX FT /note= "No start and stop codon"
XX PN US2003229914-A1.
XX XX
XX PD 11-DEC-2003.
XX XX
XX PF 21-AUG-2002; 2002US-00224880.
XX XX
XX PR 20-NOV-1998; 98US-0109283P.
XX PR 19-NOV-1999; 99US-00443041.
XX XX
XX PA (FAMO/) FAMODU O O.
XX PA (OROZ/) OROZCO E M.
XX PA (RAPA/) RAPALSKI J A.
XX PA (SHEN/) SHEN J B.
XX XX
XX PI Famodu OO, Orozco EM, Rafalski JA, Shen JB;
XX XX
XX DR WPI; 2004-052051/05.
XX DR P-PSDB; AD119003.
XX XX
XX FT New polynucleotide encoding a transcription factor polypeptide, useful in
XX FT genetic mapping for plant breeding.
XX PS Claim 2; SEQ ID NO 23; 43pp; English.
XX XX
XX CC The invention relates to a polynucleotide which encodes a transcription
XX CC factor. The nucleic acid fragment is useful in genetic mapping for plant
XX CC breeding. The present sequence is sterol-C5-desaturase cDNA.
XX XX
XX SQ Sequence 911 BP; 222 A; 214 C; 217 G; 258 T; 0 U; 0 Other;

Query Match 6.4%; Score 187; DB 12; Length 911;
Best Local Similarity 59.8%; Pred. No. 2e-33;
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

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DB 134 CCTTTTACTGTGCTCTTCCAACTTTATCTGAGTATATGATCGAGAGTGGATGGACCCGG 193
QY 2143 TGTACTCTACACTTGACCAATTCAACTGGTTCCTCTGTTTCTCTACATAGCTCTCTAT 2202
DB 194 TGTACTCTTAATATACGCGAAATGGGTTTTTCTGCATACCTTTGTTATATGGCTATAT 253
QY 2203 CTGTGTTTACTGTGAGTTTATGATTTTGGTTTCACAAAGAGCTTCATGACATTAATTT 2262
DB 254 CTCAATTTTGGGAGTTTGAATTTTACTGTGATGACAGAGTTGATGACATTAAGCCA 313
QY 2263 CTCTATAAGCATCTCCATGTACCCATCATATGTACAAAGCAAAACACACTCTCTCCA 2322
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DB 374 TTTGC----- 378
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DB 408 TTCTGCAAGCGATACCGCATGTGCTTTGGGCTCTTCTCTCTCCCAAGCACTTCAGGACGC 467
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DB 528 GCAAGGTATGGCCAGTCATGGGCGCTGGGTATCACACCATCCACCATACGACTTACCGCC 587
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DB 588 ACAACTATGGCCACTACACCGCTCTGGATGGACTGGATGTTGGTAGCT 636

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 10: gb\_gsa2:  
 11: gb\_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 24	197.2	6.7	927	8	DR584230	DR584230 WS0335.C2
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C 29	184.8	6.3	720	6	CD436598	CD436598 EL01N0360
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C 32	183.4	6.3	846	8	DR469736	DR469736 WS00948.B
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## ALIGNMENTS

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 SAIL 1124\_H08.v1, genomic survey sequence.  
 ACCESSION CL460967.1 GI:45863872  
 VERSION  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE 1 (bases 1 to 940)  
 AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D., Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.  
 TITLE A high-throughput Arabidopsis reverse genetics system  
 JOURNAL Plant Cell 14 (12), 2985-2994 (2002)  
 PUBMED 12468722  
 COMMENT Contact: Sessions A  
 Applied Trait Genetics  
 Syngenta Biotechnology Inc.  
 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA  
 Email: allen.sessions@syngenta.com  
 Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).  
 Sequences represent a pool of amplified genomic regions and not single contiguous sequences.  
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modified TAIL-PCR strategy"

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Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1247 AGTTGAGTTAAATGGTAGTAAACGCAATTTAACCTTTATTAAGTTTAAATCGTATTCAACGAA 1306
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QY 1367 GTAGCAAAATCATTTAAATATTGTAAGTTTTCCTTTCAGAAATTCGAGTACAGATCTCA 1426
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QY 1487 TTGACTTCTCGGGGTTTCAT 1507
DB 379 TTGACTTCTCGGGGTTTCAT 399

RESULT 4
BH846526
LOCUS SALK_008569.45.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_008569.45.50.x, genomic
survey sequence.
ACCESSION BH846526
VERSION BH846526.1 GI:21417397
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 328)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadranab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
T-DNA. This sequence lies within 300 bases of the 3' end of
At3g02580.
Class: T-DNA tagged.
Location/Qualifiers
1..700

source
1..328
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/scotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_008569.45.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more T-DNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 10.2%; Score 299.4; DB 9; Length 328;
Best Local Similarity 96.4%; Pred. No. 1.9e-57;
Matches 317; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 872 ATTCATGTCTCTCTCAACCTTTCCAAATATATATTTTCAAAACATTTGCTCTCTAGTTT 931
DB 1 ATTCATGTCTCTCTCAACCTTTCCAAATATATATTTTCAAAACATTTGCTCTCTAGTTT 60

QY 932 AAAACATGTAATGTTTGAATGATCTTTGCAAGACTCCATTTTGTTTAAGGTAACCTTG 991
DB 61 AAAACATGTAATGTTTGAATGATCTTTGCAAGACTCCATTTTGTTTAAGGTAACCTTG 120

QY 992 AATCTCATAGATTGTCGATTTGTTGTTATTTCCATTTTCAGGTACGTTCTGTAGACTGTA 1051
DB 121 AATCTCATAGATTGTCGATTTGTTGTTATTTCCATTTTCAGGTACGTTCTGTAGACTGTA 180

QY 1052 GTCTTGCTGACCAAGTCGGCTTAACACCCCAAAATTTCAAGATCTCACCAATCAAAATG 1111
DB 181 GTCTTGCTGACCAAGTCGGCTTAACACCCCAAAATTTCAAGATCTCACCAATCAAAATG 240

QY 1112 CTGGCTGGCCCCAATATATAGATGGCCAGTTAATCCGTCAGCTTTACTCTTTAGACCT 1171
DB 241 CTGGCTGG-CCCAATATATAGATGGCCAGTTAATCCGTCAGCTTTACTCTTTAGACCT 299

QY 1172 ACCTTAGACAGTTAGACACCTGCTAATTA 1200
DB 300 ACCTTAGACAGTTAGACACCTGCTAATTA 328

RESULT 5
BH956101
LOCUS odg94b06.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BH956101
VERSION BH956101.1 GI:23437328
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 700)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg94 row: b column: 06
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1..700

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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/notes="Vector: pORW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO100DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

```

## ORIGIN

```

Query Match          9.8%; Score 285.6; DB 9; Length 700;
Best Local Similarity 83.0%; Pred. No. 3.1e-54;
Matches 365; Conservative 0; Mismatches 64; Indels 11; Gaps 3;

QY 2397 ATGTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGAGGGATCTTCAGGCTATA 2456
Db 52 AAGTTTTCGGGTTTTCAGGGCTTCGTTCCATCCATTGGATGATCTTCAGGCAGTA 111
QY 2457 CGCAGCGTATAGCGCTGTTTATAGTGGCGATTCTCTCATACACATCTGAGTCTTTTG 2516
Db 112 CGCATGTGTAGTCTCTGTTTCATAGTCCGATACATCTCATACACATTTGAGTCTTTT 171
QY 2517 TTTTTCGAGGGATATGGACAGCAAGCATCCATGTTGTCATACATGTAACATCTGCGCT 2576
Db 172 ATTATGGAAGGGATATGGACAGTGGCAACCATGATGTCATCATGTAACATATGGCT 231
QY 2577 ATAATGGGTGCGAGTACCATACATACACATACCAACATACCAAGCATAACTATGTCAT 2636
Db 232 ATAATGGGTGCGAGCACACCATACATACACATACCAACATACCAAGCATAACTATG 291
QY 2637 TATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2696
Db 292 TATACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351
QY 2697 AGTTTCAAGGAGAAAGAAAGTGGAGATGTTCAATGCTCAGATGATTTT-----CTTC 2748
Db 352 AGCTTTAATAGAAAGAAAGTGA-TATGTTCAACGTACACATTTTTTTTGTGTCCTTC 410
QY 2749 ATATGTTGCTCTCTCGTGACTCTTATTAACACTTTCTAATCAGTCTGGTGGAAATAA 2808
Db 411 ATGTGTTTTTCTACTCTCTGAGTCTTA--AACCTTTGTAATATCAGTCTTTGTAATAA 468
QY 2809 AACATGACTGCAATAATTTGA 2828
Db 469 AACATGATGCACTATTAGA 488

```

```

RESULT 6
CB255600          326 bp mRNA linear EST 31-DEC-2004
LOCUS
DEFINITION
CB255600          36-E018428-019-008-G10-T7R MP12-ADIS-019 Arabidopsis thaliana cDNA
clone MP12p768G108Q 5-PRIME, mRNA sequence.
CB255600.1 GI:56916225
EST.
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 326)
REFERENCE
Jakoby,M., Stracke,R., Soerensen,T.R. and Weisshaar,B.
Arabisopsis thaliana cDNA library enriched in transcription factors
Unpublished (2003)
Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de

```

```

Insert Length: 326 Std Error: 0.00
Plate: 8 row: G column: 10
Seq primer: T7R; CTAATAGACTCACTATAGGA.
Location/Qualifiers
1..326
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/cultivar="At7"
/db_xref="GABI:596808"
/db_xref="taxon:3702"
/clone="MP12p768G108Q"
/tissue_type="hypocotyl"
/dev_stage="tissue culture"
/lab_host="E. coli DH5alpha mcr"
/clone_lib="MP12-ADIS-019"
/notes="Vector: pSPORT1; Site 1: NotI primer adapter;
Site 2: SalI primer adapter; RNA from cellucyte (At7) 5
days after inoculation treated with 0.002 mM cycloheximid
for 2 h in the dark. Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de. This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

```

## ORIGIN

```

Query Match          9.7%; Score 284.4; DB 6; Length 326;
Best Local Similarity 97.7%; Pred. No. 5.2e-54;
Matches 299; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 697 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 756
Db 9 TGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 67
QY 757 GACAGCTTCAGAAAGACAGAGTGAGAAAGTGGGCTTTGTTCTTCTCTCTCTCTCTCT 816
Db 68 GACAGCTTCAGAAAGACAGAGTGAGAAAGTGGGCTTTGTTCTTCTCTCTCTCTCTCT 127
QY 817 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 876
Db 128 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 187
QY 877 TGTGCTCTCTCAACCTTTCATATATATGTTTACAAATGCTGCTGCTGCTGCTGCTGCT 936
Db 188 TGTGCTCTCTCAACCTTTCATATATATGTTTACAAATGCTGCTGCTGCTGCTGCTGCT 247
QY 937 ATGTAAGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 996
Db 248 ATGTAAGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
QY 997 CATAGA 1002
Db 308 CATAGA 313

```

```

RESULT 7
CB255600          1016 bp DNA linear GSS 01-APR-2004
LOCUS
DEFINITION
CB255600          SAIL 508_H08.v1 SAIL Collection Arabidopsis thaliana genomic clone
clone SAIL_508_H08.v1, genomic survey sequence.
CB255600.1 GI:45969313
ACCESSION
CB255600          SAIL 508_H08.v1, genomic survey sequence.
VERSION
CB255600          SAIL 508_H08.v1, genomic survey sequence.
KEYWORDS
SOURCE
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1016)
REFERENCE
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mittel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
TITLE
JOURNAL

```



PUBMED  
COMMENT

12468722  
Contact: Sessions A  
Applied Trait Genetics  
Syngenta Biotechnology Inc.  
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA  
Email: allen.sessions@syngenta.com  
ABRC Stock Number CS821429; T-DNA left border flanking sequences of  
Syngenta Arabidopsis Insertion Library (SAIL) lines are available  
through the Arabidopsis Biological Resource Center (ABRC).  
Sequences represent a pool of amplified genomic regions and not  
single contiguous sequences.  
Class: TDNA tagged.

FEATURES  
source

Location/Qualifiers  
1..1016  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/scoType="Columbia"  
/db\_xref="taxon:3702"  
/clone="SAIL\_508\_H08.v1"  
/note="T-DNA left border sequences were isolated using a  
modified TAIL-PCR strategy"

## ORIGIN

Query Match 9.7%; Score 283.8; DB 10; Length 1016;  
Best Local Similarity 99.0%; Pred. No. 8.5e-54;  
Matches 296; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
QY 1378 TTTAAATATGTAAGTTGCTTTCATTCGAAATGTAGCTACAGATCTCAAGCTCTCT 1437  
DB 80 TTTAAATATGTAAGTTGCTTTCGAAATGTAGCTACAGATCTCAAGCTCTCT 139  
  
QY 1438 GTTGGCCATCTCTCTTAACAAAGCATAGTAACACTTGGACCAAGTTTGACTTCTCG 1497  
DB 140 GTTGGCC-TATCTCTCTTAACAAAGCATAGTAACACTTGGACCAAGTTTGACTTCTCG 198  
  
QY 1498 GCGGTTTACGCGGCGACTATGGCAGATTATAATGATCAGATCGTCAATGAGACTCTT 1557  
DB 199 GCGGTTTACGCGGCGACTATGGCAGATTATAATGATCAGATCGTCAATGAGACTCTT 258  
  
QY 1558 TTTTAAACCGAATGTTCTGAGTCACTTTTCGCGGTGAATCTATGGGAACCTTTACCAC 1617  
DB 259 TTTTAAACCGAATGTTCTGAGTCACTTTTCGCGGTGAATCTATGGGAACCTTTACCAC 318  
  
QY 1618 ATTTCTCCAGACATGGCTCCGGAACCTACCTCCGGAACCATATCTTCACTCTCC 1676  
DB 319 ATTTCTCCAGACATGGCTCCGGAACCTACCTCCGGAACCATATCTTCACTCTAC 377

## RESULT 8

CD822918  
LOCUS  
DEFINITION  
CD822918  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Brassica napus (rape)

749 bp mRNA linear EST 10-JUL-2003  
BN25.047B03F020109 BN25 Brassica napus cDNA clone BN25047B03, mRNA  
sequence.  
CD822918  
CD822918.1 GI:32504858  
EST.

## REFERENCE

1 (bases 1 to 749)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

FEATURES  
source

and <http://genoplante-info.infobiogen.fr>.  
Location/Qualifiers  
1..749  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"  
/clone="BN25047B03"  
/tissue\_type="seed"  
/clone\_lib="BN25"

## ORIGIN

Query Match 9.6%; Score 281.6; DB 6; Length 749;  
Best Local Similarity 73.0%; Pred. No. 2.6e-53;  
Matches 419; Conservative 0; Mismatches 69; Indels 86; Gaps 1;  
  
QY 1973 TGTGGTCTTAGTCTTATTTCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2032  
DB 239 TGTGGTCTTCTTATATCTTATTAACCTTAAGCTCAAGCTTTACTTCCCAAGATTCAATTC 298  
  
QY 2033 CTACGAGAAAGCAATGCTTTTGCATAATATAGTGGCAATGAAGGCTATGCTTGGTACA 2092  
DB 299 CTACAAAGAAAGCGGATGATTATGCAATACATGTGCAATGAAGCTATGCTTGGTACA 358  
  
QY 2093 CTCTCTTCTCCAGCTGCTCTGATATATGATCGAGCATGGTTGGACCAATGTTACTCTA 2152  
DB 359 CACTTCTTCCAACTGCTCTCCGAGTATATGATCGAGCGTGGTTGGACCAATGTTACTCTA 418  
  
QY 2153 CACTTGGACCATTTCAACTGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2212  
DB 419 CACTTGGACCATTTCAACTGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478  
  
QY 2213 TTGAGTTTATGATTTTATTTGGGTTTCAAGAGCTTTCATGACATTAATTTCTCTATAAGC 2272  
DB 479 TTGAGTTTATGATTTTATTTGGGTTTCAAGAGCTTTCATGACATTAATTTCTCTATAAGC 538  
  
QY 2273 ATCTCCATGCTACCCATCATATATGTAACAAGCAAAACACACTCTCTCTCAATTTGCCGTA 2332  
DB 539 ATCTCCATGCTACCCATCATATATGTAACAAGCAAAACACACTCTCTCTCAATTTGGCT 594  
  
QY 2333 TGTCAAAGCTATATGTTCTCAATCTAAATTCAAGAGCTTGTATCAATGGTGACTTCTTTA 2392  
DB 595 -----  
  
QY 2393 CTGTGATTTTTCGGGTTTTCAGGCTCGCATTCATTCGCTGGACGGGATCTTCAGGC 2452  
DB 595 -----GGGCTCGGTTCCATCTTTGGACGGGATCTTCAGGC 632  
  
QY 2453 TATACCGCAGTGATAGCGCTGTTTATAGTCCGATTCATCTCATAAACACATCTGAGTCT 2512  
DB 633 AGTACCGCAGTGATAGCTCTGTTTCAATTTGCAATTCATCTCATAAACGATCTGAGTCT 692  
  
QY 2513 TTTGTTTTTGGAGGGATATGACAGCAAGCATC 2546  
DB 693 TTTGTTTTTGGAGGGATATGACAGCAAGCATC 726

## RESULT 9

BZ384971/c  
LOCUS  
DEFINITION  
BZ384971  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 327)  
Alonso,J.M., Leisese,T.J., Barajas,P., Chen,H., Cheuk,R.,

**TITLE**  
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shinn, P., Zimmerman, J. and Ecker, J.R.  
**JOURNAL**  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
**COMMENT**  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated intron of At3g02580.  
**Class:** TDNA tagged.

**FEATURES**  
source  
1. .327  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/scot\_type="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_136266.46.25.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at http://signal.salk.edu/tdna\_protocols.html"

**ORIGIN**  
Query Match 9.5%; Score 278.4; DB 9; Length 327;  
Best Local Similarity 99.6%; Pred. No. 1.2e-52;  
Matches 279; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTTTGGTATTATTGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT 60  
|||||  
Db 280 GTTTGGTATTATTGATGACAGAGAGCTTCATGACATTAAGCCCTCTCTATAAGTATCT 221  
|||||  
QY 61 CCATGCCACCATCATATCTACAAAGAGAGATACATCTCTCCATTTGCCGGTAAGTG 120  
|||||  
Db 220 CCATGCCACCATCATATTTACAAAGAGAGATACATCTCTCCATTTGCCGGTAAGTG 161  
|||||  
QY 121 TTTTCAGTTGTTCTCTTTAGTTCTTTGTAAGAGTTGTTAGTATTTCTTACCAG 180  
|||||  
Db 160 TTTTCAGTTGTTCTCTTTAGTTCTTTGTAAGAGTTGTTAGTATTTCTTACCAG 101  
|||||  
QY 181 AAAAGACTTTGTGACGAGCTGTTGTACTCCAAATCACATTTTGCAATTCCTTATCCATAA 240  
|||||  
Db 100 AAAAGACTTTGTGACGAGCTGTTGTACTCCAAATCACATTTTGCAATTCCTTATCCATAA 41  
|||||  
QY 241 AGTAACACAGAGAGCTAGAAATTAATATGTCAGCTGCA 280  
|||||  
Db 40 AGTAACACAGAGAGCTAGAAATTAATATGTCAGCTGCA 1  
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**RESULT 10**  
CD823327  
LOCUS  
DEFINITION  
BN25.048G14F020110 BN25 Brassica napus cDNA clone BN25048G14, mRNA  
sequence.  
ACCESSION  
CD823327  
VERSION  
CD823327.1 GI:32505267  
KEYWORDS  
EST.  
SOURCE  
Brassica napus (rape)  
ORGANISM  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 482)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Unpublished (2003)  
Contact: Genoplatte  
Genoplatte, a major partnership french program in plant genomics  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00

**COMMENT**

Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

**FEATURES**

source  
1. .482  
Location/Qualifiers  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"  
/clone="BN25048G14"  
/tissue\_type="seed"  
/clone\_lib="BN25"

**ORIGIN**

Query Match 9.1%; Score 265.4; DB 6; Length 482;  
Best Local Similarity 84.5%; Pred. No. 1.2e-49;  
Matches 310; Conservative 0; Mismatches 56; Indels 1; Gaps 1;  
QY 462 TTTACAGGCTTGCAATTCACCCAGTAGAGCGGATCTTAAGCTGTACCCGATGTGATAG 521  
|||||  
Db 29 TTGCCGGGCTTGCGTTTCACCCAGTAGATGGATTCTTCAGGCTTTACCGCATGTGATAG 88  
|||||  
QY 522 CGCTG-TTATAGTGCATTCATTTTCACAACTCATATAGTCTTTTGTTCATGGAGCGCA 580  
|||||  
Db 89 CTCTCTTTATAGTGCATTCATTTTCACAACTCATATAGTCTTTTGTTCATGGAGCGCA 148  
|||||  
QY 581 TATGACGCGGAACATCCATGACTGCATCCATGCAACATCTGGCCAGTAATGGGTGCAG 640  
|||||  
Db 149 TATGACGCGGAACATCCATGACTGCATCCATGCAACATCTGGGTGTATGGGTGCAG 208  
|||||  
QY 641 GATACCATCAGTATACACCAAGAGATACCAAGCATTAAGCTCATTTATACATATGA 700  
|||||  
Db 209 GGTACCATCAGTATACACCAAGAGATACCAAGCATTAAGCTCATTTATACATATGA 268  
|||||  
QY 701 TGGATTGATGTTGGCTCTCTTAGGGATCCCTCTTTAGAGAGATGACACCAAGACA 760  
|||||  
Db 269 TGGATTGATGTTGGCTCTCTTTAAAGACCCCTCTTTTGAAGATGTTGACAAAGACA 328  
|||||  
QY 761 GCTTCAAGAAAGCAGAGTGAAGTCCCACTGGGTTTTTGTCTCTCTTTGTCTTTGTG 820  
|||||  
Db 329 TCTCCAGAAAGCAGAGTGAAGTCCCTTTTGTCTCTCTTTGTCTCTTTGTCTTTT 388  
|||||  
QY 821 TTGTTGT 827  
|||||  
Db 389 TTACTTT 395  
|||||

**RESULT 11**

CD834242  
LOCUS  
DEFINITION  
BN45.041B07F011207 BN45 Brassica napus cDNA clone BN45041B07, mRNA  
sequence.  
ACCESSION  
CD834242  
VERSION  
CD834242.1 GI:32516182  
KEYWORDS  
EST.  
SOURCE  
Brassica napus (rape)  
ORGANISM  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 644)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Unpublished (2003)  
Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00



Db 335 GGTAAAGGTGTGGCTGTAAATGGTGGCGGCTATCATACCAATTCACCATACCAACATACCGC 276

Qy 2622 CATAACTATGCTCATATATACCATATGATGAGTGGAGCTGATGTTGGCTCTCTATGGTTCT 2681

Db 275 CATAATATGCTCATATACCATATGATGAGTGGAGCTGATGTTGGAACTCTACGTGATCC 216

Qy 2682 TTAGCAGAAAAGACA 2697

Db 215 GTTGAAGAGGATGCCA 200

## RESULT 13

## CK269990

## LOCUS

DEFINITION EST716068 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POACQ30 5' end, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

CK269990 920 bp mRNA linear EST 03-AUG-2004  
EST716068 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POACQ30 5' end, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

1. .920  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
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/tissue\_type="abiotic stress treated leaf and root tissue"  
/lab\_host="DH10B-TonA"  
/clone\_lib="potato abiotic stress cDNA library"  
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

## ORIGIN

Query Match 7.8%; Score 228.4; DB 7; Length 920;  
Best Local Similarity 62.7%; Pred. No. 4e-41;

Matches 424; Conservative 0; Mismatches 166; Indels 86; Gaps 1;

Qy 2022 AGAATCCATTCTCTACGAGAAAGCAATGCTTTTGGAAAATATACGTGGCAATGAAGCTAT 2081

Db 304 AGATGCCATACCATCAAGGAAGCAATGCTCTTGGAAATATCAGTTGCTATGAAAGCTAT 363

Qy 2082 GCCTTGGTACACTCTTCTCCAGCTGTCTCTCAGTATATGATCGAGCATGGTTGGACCAA 2141

Db 364 GCGGTGGTACTGTGCGCTTCCATCTTCTGAGTACATGATTTGAAACGGATGGACCAA 423

Qy 2142 ATGTTACTCTACACTTGGACCAATTTCACTGGTTCCTCTCTCTCTCTACATAGCTCTCTA 2201

Db 424 ATGTTTTTGGGAGATAAGTGATGTTGGATGGCTTACCTACATCATCAATTCGCGCTATTTA 483

Qy 2202 TCTGTTTTTGTAGTTGATTTATCATTTTATTTGGGTTCACAAAGAGCTTCATGACATTAAT 2261

Db 484 TCTCGTAATATGTTGGAGTTTGGAAATCTACTGGATGCAAAAGTTGTTGTCATGACATAAACC 543

Qy 2262 TCTCTATAAGCATCTCCATGTCCATCATCATATGATACAAAGCAAAACACACTCTCTCC 2321

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Db 604 GTTTCGTGGATTG----- 616

Qy 2382 TGACTTCTTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCATTCCTCCGCTGGACGG 2441

Db 617 -----GCATTCACCCATTTGGATGGA 637

Qy 2442 ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTCCGATTCATCTCATPACA 2501

Db 638 ATACTTCAGGCTATACCGCACGTGATAGCGCTGTTTATAGTCCGATTCATCTCATPACA 697

Qy 2502 CATCTGAGTCTTTGTTTGGAGGATATGACAGCAGCATCCATCATGATTCATCAT 2561

Db 698 CACATAGCGCTCATATTTTGGAGCGCTTATGAGCGCTTAATTTTCCATGACTGCATACAT 757

Qy 2562 GGTAAACATCTGGCTTATTAATGGTGCAGGATACCATACCATACACCATACACATACAAG 2621

Db 758 GGTAAAGTGTGGCTTGTATGGTGGCTGATATACATATGATGGATGGATGGATGGATGG 817

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Db 818 CATAATTTATGGTCAATTACACAATATGATGGATGGATGGATGGATGGATGGATGGAT 877

Qy 2682 TTAGCAGAAAAGACA 2697

Db 878 GTTGAAGAGGATGCCA 693

## RESULT 14

## CK264499

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

CK264499 924 bp mRNA linear EST 03-AUG-2004  
EST710577 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POABT06 5' end, mRNA sequence.

CK264499  
CK264499.1 GI:39821477  
EST.

Solanum tuberosum (potato)  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 924)  
Buell, C.R., Hart, A., Ziemann, V., Karamycheva, S.A. and Baker, B.  
Generation of ESTs from abiotic stressed potato tissue  
Unpublished (2003)

Other ESTs: EST710578  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>  
 Seq primer: ATT TAG GTG ACA CTA TAG.

# FEATURES

Location/Qualifiers  
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 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="POAST06"  
 /tissue\_type="abiotic stress treated leaf and root tissue"  
 /lab\_host="DH10B-Tona"  
 /clone\_lib="potato abiotic stress cDNA library"  
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 7.8%; Score 227; DB 7; Length 924;  
 Best Local Similarity 62.7%; Pred. No. 8.3e-41;  
 Matches 422; Conservative 0; Mismatches 165; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCTTCCAGGCAATGCTTTTGGCAATATACGTTGGCAATGAAGCTAT 2081  
 DB 338 AGATGCCATACCATCAAGAGCAATGCTTCTGCAATATCAGTTGCTATGAAGCTAT 397

QY 2082 GCCTTGGTACATCTTCTCCAGCTCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141  
 DB 398 GCGTGGTACTGTGCGCTTCCATCACTTTCTGAATACATGATGGAACGGATGGACCA 457

QY 2142 ATGTTACTCTACACTTGACATTTCAACTGGTTCTCTGTTCTCTCTACATAGCTCTCTA 2201  
 DB 458 ATGTTTGGAGNATAGTGTGATGTTGGATGGCTACCTACATCATCATGCGCTATTTA 517

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 DB 518 TCTTGTAAATAGTGGAGTTTGGAACTCTACTGGATGCAAAAGTTGTTGATGACATAAACC 577

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 DB 578 TCTGTACAAATATCTGCTGCTACATCATATTTTACACAGCAACACACTTTTCCC 637

QY 2322 ATTTGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381  
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QY 2382 TGACATCTTTTACTGTAGTTTTCGGGTTTTCAGGCTCGCAATCCATCCGCTGACGGG 2441  
 DB 651 -----GCATTCACCCATTTGGATGA 671

QY 2442 ATACTTCAGGCTATACCGCAGTATAGCGCTGTTTATAGTCCGATTCATCTCTACA 2501  
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QY 2502 CATCTGAGTCTTTTGTGTTTGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561  
 DB 732 CACATAGCACTCATATTCCTGGAAGCCTTATGACAGCTAATATTCATGACTGCATACAT 791

QY 2562 GGTAACTCTGCGCTATATATGTTGCGAGGATACCATACATACACCATACATACAG 2621  
 DB 792 GGTAAAGGTGTCCTGTTAATGTTGCGCTATATACATACATTCACCATACATACAG 851

QY 2622 CATTAATGTTGTCATTAACCATATGATGAGTGGTCTGTTGGCTCTCTTATGTTCT 2681  
 DB 852 CATTAATGTTGTCATTAACCATATGATGAGTGGTCTGTTGGTCTCTTATGTTCT 911

QY 2682 TTAGCAGAAAAG 2694  
 DB 912 GTTGAAGAGGATG 924

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 ACCESSION CN731853  
 VERSION CN731853.1 GI:65289668  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 753)  
 AUTHORS Xiang, D., Venglat, P., Keller, G., Selvaraj, G. and Batla, R.  
 TITLE Gene Expression Patterns during Brassica Zygotic Embryogenesis  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Raju Batla  
 Molecular and Developmental Genetics  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 5267  
 Fax: 306 975 4839  
 Email: Raju.Batla@nrc-cnrc.gc.ca  
 High quality sequence stop: 753.  
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 /mol\_type="mRNA"  
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 /note="Vector: pDNR-LIB CREATOR; Site 1: Sfi I A; Site 2:  
 Sfi I B; Zygotic embryos at heart stage from Brassica  
 napus seeds were used for the isolation of PolyA RNA and  
 in the construction of the cDNA library. Sequences have  
 been trimmed to remove vector and low quality regions  
 using LUCY sequence cleanup software (www.tigr.org)."

ORIGIN

Query Match 7.7%; Score 226.6; DB 7; Length 753;  
 Best Local Similarity 69.2%; Pred. No. 9.9e-41;  
 Matches 370; Conservative 0; Mismatches 79; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCTTACGAGAAAGGCAATGCTTTTGGCAATATACGTTGGCAATGAAGCTAT 2081  
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QY 2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGTTGGACCAA 2141  
 DB 365 GCCTTGGTACACTCTGCTTCCAACTGTATCTGAGTATATGATTGAAAGTGGATGACTAA 424

QY 2142 ATGTTACTCTACACTTTGACCACTTTCAACTGGTTCTCTGTTCTCTCTACATAGCTCTCTA 2201  
 DB 425 ATGTTACTCGAGTAGGCGAAGTCAGCTGGATCTCTACTTGTGTTCAATCGGACATA 484

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Qy 2202 TCTGTGTTTGTAGTTGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
Db |||||
Qy 485 TCTGTGTTTGTAGTTGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAGCC 544
Db |||||
Qy 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAACAGCAAAACACACTCTCTCC 2321
Db |||||
Qy 545 TCTCTATAAGTAATCTCCATGCCACCCATCATATCTACAACAAACAGATACACTCTCTCC 604
Db |||||
Qy 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
Db |||||
Qy 605 CTTTGGC----- 611
Qy 2382 TGACTTCTTTTACTTGTATGTTTTTCGGGTTTTCAGGGCTCGCATTCATCCGCTGGACGGG 2441
Db |||||
Qy 612 -----GGGCTTGGGTTTCACCCACTAGACGGG 638
Qy 2442 ATACTTCAGGCTATACCGACGTTAGCGCTGTTTATAGTCCGATTCATCTCATPAACA 2501
Db |||||
Qy 639 ATACTTCAAGCTGTACCGACGTTGTTGCTTTGTTTATAGTCCGATTCATTTCAACAAC 698
Qy 2502 CATCTGAGTCTTTTGTGTTTGGAGGGATATGGACAGCAAGCATCCATGATTGCA 2556
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Job time : 11155 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	15.8	1175	3	US-09-885-723-23
2	203.4	7.0	1447	3	US-09-443-041A-27
3	188	6.4	1210	3	US-09-443-041A-29
4	187	6.4	911	3	US-09-443-041A-23
5	179.6	6.1	1318	3	US-09-443-041A-25
6	173.8	5.9	1070	3	US-09-443-041A-9
7	118.4	4.0	300	3	US-09-313-294A-4514
8	90.8	3.1	269	3	US-09-313-294A-379
9	90	3.1	459	3	US-09-443-041A-13
10	82.8	2.8	314	3	US-09-313-294A-7458
11	77.8	2.7	7218	2	US-08-232-463-14
12	71	2.4	495	3	US-09-443-041A-15
13	69.4	2.4	360	3	US-09-443-041A-11
C 14	68	2.3	612	3	US-09-902-540-1357
C 15	60.6	2.1	614	3	US-09-902-540-1318
16	60.6	2.1	1141	3	US-09-806-708B-22
C 17	59.6	2.0	1039	3	US-09-902-540-1280
18	56.8	1.9	2039	3	US-09-949-016-2275
19	56.8	1.9	2092	3	US-09-949-016-901
20	56.2	1.9	396	3	US-09-640-173-53
21	56.2	1.9	396	3	US-09-713-550-53
22	56.2	1.9	396	3	US-09-825-294-53
23	56.2	1.9	396	3	US-09-970-966-53
C 24	55.2	1.9	19124	2	US-08-487-826B-13

C 25	53.8	1.8	240	2	US-08-628-417-6	Sequence 6, Appli
C 26	53.2	1.8	1141	3	US-09-806-708B-22	Sequence 22, Appl
C 27	52.8	1.8	4167	3	US-09-973-278-700	Sequence 700, App
28	52.8	1.8	9277	3	US-09-949-016-14017	Sequence 14017, A
29	52.8	1.8	21168	3	US-09-949-016-12643	Sequence 12643, A
C 30	51.4	1.8	2447	2	US-09-014-969-14	Sequence 14, Appl
C 31	51.2	1.8	1098	3	US-09-614-221A-113	Sequence 113, App
C 32	50.8	1.7	1696	3	US-09-835-811-1	Sequence 1, Appli
C 33	50.2	1.7	658	3	US-08-998-416-595	Sequence 595, App
C 34	49.4	1.7	41736	3	US-09-949-016-17091	Sequence 17091, A
C 35	49	1.7	282	3	US-09-621-976-18648	Sequence 18648, A
36	48.8	1.7	832	3	US-09-621-976-2813	Sequence 2813, Ap
37	48.6	1.7	5852	2	US-07-867-106-2	Sequence 2, Appli
C 38	48.2	1.6	145241	3	US-09-949-016-17394	Sequence 17394, A
C 39	48.2	1.6	145241	3	US-09-949-016-17395	Sequence 17395, A
C 40	48	1.6	237510	3	US-09-949-016-14273	Sequence 14273, A
C 41	47.8	1.6	1662	3	US-09-668-097A-13	Sequence 13, Appl
C 42	47.8	1.6	50000	3	US-09-662-254B-25	Sequence 25, Appl
43	47.8	1.6	54033	3	US-09-949-016-12091	Sequence 12091, A
44	47.8	1.6	54033	3	US-09-949-016-14325	Sequence 14325, A
C 45	47.6	1.6	603	3	US-09-248-796A-5211	Sequence 5211, Ap

ALIGNMENTS

RESULT 1  
US-09-885-723-23  
; Sequence 23, Application US/09885723  
; Patent No. 6822142  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS  
; FILE REFERENCE: MTC6783.1  
; CURRENT APPLICATION NUMBER: US/09/885,723  
; CURRENT FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 1175  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-885-723-23

Query Match 15.8%; Score 461; DB 3; Length 1175;  
Best Local Similarity 97.6%; Pred. No. 3e-108;  
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY	462	TTTACAGGGCTTGCA-TTCACCCAGTAGACGGGATACTTAAGGCTGTACCGCATGTGATA	520
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QY	521	CGGCTG-TTATAGTGCCAAATTCATTTCACTACTATAGGCTCTTTTGTTCATGGAAGG	579
Db	703	CGGCTGTTTATAGTGCCAAATTCATTTCACTACTATAGGCTCTTTTGTTCATGGAAGG	762
QY	580	ATATGAGCGGCGAAACATCCATGACTGTCATCCATGGCAACATCTGCCAGTATATGGGTGCA	639
Db	763	ATATGAGCGGCGAAACATCCATGACTGTCATCCATGGCAACATCTGCCAGTATATGGGTGCA	822
QY	640	CGATACCATACGATACACACACGACATACAGCATATATATGTCATATACCATATG	699
Db	823	CGATACCATACGATACACACACGACATACAGCATATATATGTCATATACCATATG	882
QY	700	ATGATGTTGGATGTTGGCTCTCTTAGGGATCTCTCTTAGAGAGAGATGACAAACAGAC	759
Db	883	ATGATGTTGGATGTTGGCTCTCTTAGGGATCTCTCTTAGAGAGAGATGACAAACAGAC	942
QY	760	AGCTTCAAGAAGCAGAGTGAATATGCCACTTGGGTTTGTCTTCTCTTGTCTTGTCTTGT	819
Db	943	AGCTTCAAGAAGCAGAGTGAATATGCCACTTGGGTTTGTCTTCTCTTGTCTTGTCTTGT	1002
QY	820	GTTGTTGTTGTTCAAGTTTTCAGCCTTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT	879





Qy	2503	ATCTGAGTCTTTTGTGTTTGGAGGAGATATGGACACGACGATCCATCGATGTCATACATG	2562
Db	468	ACATCCCTCTCGTGTCTTTGGAGGGCGTGTGGACGCAAAACATCCACGATCGATTCACG	527
Qy	2563	GTAACATCTGGCCCTATAATGGGGTGCAGGATACCATACCATAACCCATACAACATACAAGC	2622
Db	528	GCAAGGTATGGCCAGTCATGGGGCGCTGGGTATCACACCATCCACCATACGACTTAACGCC	587
Qy	2623	ATAACTATGGTCAATTATACCATATGGATGGACCTGGATGTTTGGGCTCTCT	2671
Db	588	ACAACATATGGCCACTACACCGTCTGGATGGACTTGGATGTTTGGTACGCT	636

## RESULT 5

```

US-09-443-041A-25
; Sequence 25, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafaleki, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443, 041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-443-041A-25

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Query Match 6.1%; Score 179.6; DB 3; Length 1318;  
Best Local Similarity 58.8%; Pred. No. 6.3e-36;  
Matches 389; Conservative 0; Mismatches 189; Indels 86; Gaps 1;

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591	Db	ATTGTACAAGTACCTCGACACATACCACCATATTTACACAGAGAGTATACCTTATCACC	650
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656	Db	-----CAGGACTAGCATTTCCATCCACTGGATGGG	684
2442	QY	ATACTTTCAGGCTATACCGCACGATGATAGCGCTCTTTATAGTGGCGATTCATCTCATAAACA	2501
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RESULT 4
US-09-443-041A-23
; Sequence 23, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 911
; TYPE: DNA
; ORGANISM: Zea mays
US-09-443-041A-23

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Query Match 6.4%; Score 187; DB 3; Length 911;  
Best Local Similarity 59.8%; Pred. No. 6.7e-38;  
Matches 388; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

2023	QY	GAATTCATTCTCTACGAGAAAGCAATGCTTTTGTGCAATATATACGTGGCAATGAAAGGCTATG	2088
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74	Db	GATGCCATCCCACAAATGAAGCTATGAAGAAAGCAATAGCTGTAGCATCCAGGCTATG	133
2083	QY	CCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATTCGAGCAATGTTGGACCAAA	2142
	Db		
134	Db	CCTTTTACTGTGCTCTTCTCCAACTTTATCTGAGTATATGATTCGAGAGTGTGATGGAACCCGG	193
2143	QY	TGTTACTCTACACTTGCACCAATTTCAACTGGTCTCTCTGTTTCCCTCTCATATAGCTCTCTAT	2202
	Db		
194	Db	TGTTACTTTTAATATACGCGAAATGGGTTTTTCTGCAATCCTTTGTGTTATATGGCTATGTAT	253
2203	QY	CTTGTGTTTTAGTTGAGTTTTATGATTTATTTGGGTTTCAAAAGAGCTTTCATGACATTAATAATTT	2262
	Db		
254	Db	CTCATTTTTTGTGGAGTTTGGAAATTTACTGGATGCACAGAGTTGCGATGACATAAAGCCA	313
2263	QY	CTCTATAAGCATCTCCATGCTACCCATCATATGTATCAACAAAGAAACACACTCTCTCCA	2322
	Db		
314	Db	CTATACAAACATCTGCATGCGACCCACCATTATTTACAAAGAGGAACACCTTTGTCTCCG	373
2323	QY	TTTGCCGGTATGTCAAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTTGTATCAATGGT	2382
	Db		
374	Db	TTTGC-----	378
2383	QY	GACTTCTTTACTTGATGTTTTTTTCGGGTTTTTCAGGGCTGCAATTCATTCGCTGGACGGGA	2442
	Db		
379	Db	-----TGGACTCGCGGTTTTCACCCACTGGATGGTA	407
2443	QY	TACTTCAGGCTATACCGCAGCTGATAGCGCTGTTTATAGTGGCGATTTCACTCTCATACAC	2502
	Db		
408	Db	TTCTGAAAGCGATACCGCATGTGTTGCGCTCTTCTCTCCCAACGCAATTCAGGACGC	467



:	ORGANISM:	Glycine max
US-09-443-041A-13		
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Best Local Similarity	66.8%;	Pred. No. 4.le-13;
Matches 143; Conservative	0; Mismatches	70; Indels 1; Gaps 1;
Qy	1524	GATTATTAATGATCAGATCGTCAATGAGACCTCTTTTACAAACGAATGGTTCGTAGTCAC 1583
Dd	100	GAATATTCGAGGCTGTTCGGCGAAGACACGGACTTGTACAAACGCATTTGTGTGGGGGCC 159
Qy	1584	CTTTTCGGGTGAATCTATGSGGAACCTTTTACCACATTTCTCCAGACATCGCTCCCGAAC 1643
Dd	160	CTATTGCGGCACCTCTGTGTGGGGGCCACTCCCGGCTTCTTCAGACGTGGCTTCGCAAT 219
Qy	1644	TACCTCGCGCGAAACATACTCTACTTTCATCTCCGGGTTCTCTGTGTCCTTCTACATCAT 1703
Dd	220	TACCTCGCGCGCGTTCTCCTCTIACCTCCCTCTCTGGGCTCTGTGTGGTCTCTTACATTTAT 279
Qy	1704	TA-CCTTAAACTCAACGTTTTACGTCCCCCAAAGT 1736
Dd	280	TATTGGGAAGCGCAACGTTTCATCTGCCCAAGAAT 313

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RESULT 10
US-09-313-294A-7458
US-09-313-294A-7458
; Sequence 7458, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura F.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7458
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381763H1
US-09-313-294A-7458

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	Best Local Similarity	60.8%	Pred. No. 2.4e-11		
	Matches 135	Conservative 0	Mismatches 87	Indels 0	Gaps 0
Qy	1520	GGCAGATTAAATGATCAGATCGCTCAATGAGACCTCTTTTACAAACCGAATGGTCTTGAG	1579		
Db	37	GGCGGACTACCTTTGGCGGTTCTGTGGCGGAGACAGAGTGGTACACGAGGTGTGCTCTCAG	96		
Qy	1580	TCACTTTTGGCGGTGAATCTATGGGAACTTTACCAATTTCTCTCAGACATGGCTTCG	1639		
Db	97	CGCGGTGGCGCCAGGCGCACTGTGGCGCGGCCCTGCCGCACCCGGTCAGTCATGGATGCG	156		
Qy	1640	GAACTACTCTCGCGGAAACATACTCTACTTTCATCTCGGGCTTCTCTGGTGCTTCTACAT	1699		
Db	157	CAACTGGGTGGCGGTTACCTCTCTATTTCATCTCTGGTTTCTCTGGTGCTCTCGTCAT	216		
Qy	1700	CTATTACCTTAAACTCAACGGTTTACGTCGCCAAAGGTTACTT	1741		
Db	217	CTACTACTGGAAGCGGCACGCCCTACATCCCAAGATGCCAT	258		

RESULT 11  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:



[illegible]

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RESULT 15
US-09-902-540-1318/c
; Sequence 1318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1318
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(614)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318

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NAME/Seq: unsure	2.1%;	Score 60.6;	DB 3;	Length 614;	
LOCATION: (1)..(614)	Best Local Similarity	50.2%;	Pred. No. 1.7e-05;		
OTHER INFORMATION: unsure at all n locations	Matches 150;	Conservative 0;	Mismatches 149;	Indels 0;	Gaps 0;
US-09-902-540-1318					
Qy	1736	TTACTTTTTTCCAATTCGATGTTCTGTTTTTGGAAACCTTCTTTTTTGTTGATTTCCTTCGATT	1795		
Db	600	TTTTCTTTTTTGAATTTCTTTTTTTTTTTGTTCTTTTCTTTTGTCTTCTTCTTCTTGT	541		
Qy	1796	GTATCGCCTGATAGATATGCTGTTATACGTTAAACCTTTTTTTTCTTACTGTTTACTTTCACTTC	1855		
Db	540	GTATTT	481		
Qy	1856	TTGCTCTTCTACTTCTCATTTAAATAGTTTTTAAAGTTTAAATATTTTTTGGCTAAATCCACATT	1915		
Db	480	TTCTTTTTTGTGTTT	421		
Qy	1916	TTTTTAAGTTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTTGAAATTTGT	1975		
Db	420	TTTATGTTTTTTGTGTGTTTTTT	361		
Qy	1976	GGTCTTAGTTCATTTCTTGCTGGTTCCTCTATTTTTTTTGTGGTGTAGAAATCCATTCCT	2034		
Db	360	GTATTTTTTTTTTTATTTTGTGTTTTGTTTGTGTTTTTTTTTTTTTTTGTCTTCTTTTTTTTTTCT	302		

Search completed: March 7, 2006, 13:20:15  
Job time : 509 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:24:36 ; Search time 2072 Seconds  
(without alignments)  
11673.712 Million cell updates/sec

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Perfect score: 2925  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2925	100.0	2925	7	US-10-736-318-22
3	924.4	31.6	1889	3	US-09-775-879-20
4	924.4	31.6	1889	7	US-10-736-318-20
5	461	15.8	1175	3	US-09-885-723-23
6	461	15.8	1175	9	US-10-862-907-23
7	347.2	11.9	846	3	US-09-938-842A-421
8	347.2	11.9	846	3	US-09-938-842A-421
9	203.4	7.0	1447	6	US-10-224-880C-27
10	200.8	6.9	1253	7	US-10-767-701-13122
11	189.4	6.5	833	6	US-10-259-194A-287
12	188	6.4	1135	6	US-10-259-194A-530
13	188	6.4	1210	6	US-10-224-880C-29
14	187	6.4	911	6	US-10-224-880C-23
15	184.4	6.3	828	6	US-10-259-194A-608
16	179.6	6.1	825	7	US-10-395-463-33
17	179.6	6.1	1318	6	US-10-224-880C-25
18	173.8	5.9	1070	6	US-10-224-880C-9
19	151.8	5.2	635	6	US-10-259-194A-422
20	142.4	4.9	699	7	US-10-425-114-24729
21	106	3.6	754	7	US-10-424-593-66086
22	104.6	3.6	285	7	US-09-294-093B-1568
23	93.4	3.2	404	7	US-10-425-114-5986

ALIGNMENTS

RESULT 1

US-09-775-879-22  
; Sequence 22, Application US/09775879  
; Patent No. US2002006822A1  
; GENERAL INFORMATION:  
; APPLICANT: Choe, Sunghwa  
; APPLICANT: Feldmann, Kenneth A  
; TITLE OF INVENTION: Dwf7 MUTANTS  
; FILE REFERENCE: 2225-0003  
; CURRENT APPLICATION NUMBER: US/09/775, 879  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/179,901  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 2925  
; TYPE: DNA  
; ORGANISM: Genomic HDP7  
US-09-775-879-22

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Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2925;	Conservative	0;	Mismatches	0;	
		Indels	0;	Gaps	0;
QY	1	GTTTGGTATTTATTTGGATGCGACAGAGCTTCATGACATTAAAGCTCTCTATAAGTATCT	60		
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QY	61	CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGAAGTG	120		
DB	61	CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGAAGTG	120		
QY	121	TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAAGATTGGTAGCATTTAGTTTCTTACCAG	180		
DB	121	TTTTTCAGTTTGTCTTCTTTAGTTCTTTGTAAAGATTGGTAGCATTTAGTTTCTTACCAG	180		
QY	181	AAAAGACATTTGTGACAGCTGCTGTACTCCAAATCACATTTTGGATTCCTTATCCATAA	240		
DB	181	AAAAGACATTTGTGACAGCTGCTGTACTCCAAATCACATTTTGCATTCCTTATCCATAA	240		
QY	241	AGTAAACCAAGAGGCTAGAAATATATAAATGTGACGCTGCAATTCTTACATATGTCAGAG	300		
DB	241	AGTAAACCAAGAGGCTAGAAATATATAAATGTGACGCTGCAATTCTTACATATGTCAGAG	300		
QY	301	AGACTTCTGACTTAAACACAGAGTTTAGATCTTTTGTGTTTCTCTTCTGGTCTCGGACTGATT	360		

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301 AGACTTCTGACTTAACGAGGTTTAGATCTTGTGTTCTCTCTGGTCTCGGAGTAT 360  
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Qy  
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1741 TTTTCAATTCGATGTTCTGTTTGAACCTTTCTTTTGGTGAATCTTCTGATGTTGTTGTT 1800  
Qy  
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Db  
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Qy  
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Qy  
1921 AGTTGAATCTCCATGAAATTTGAGCTCAAAATATACCAATGAATGAAATTTGTTGTTTC 1980  
Db  
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Qy  
1981 TTAGTGTCTATTTCTGTTGTTTCTTCTATTTTGGTGTAGAAATCTCTACGAGA 2040  
Db  
1981 TTAGTGTCTATTTCTGTTGTTTCTTCTATTTTGGTGTAGAAATCTCTACGAGA 2040  
Qy  
2041 AAGGCAATGCTTTTGCATAATATACGTGGCAATGAAAGGCTATGCTTTGGTACATCTTCT 2100  
Db  
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Qy  
2101 CCAGCTGTCTGTAGTATATGATCGAGCATGTTGCGAACAAATGTTACTCTACACTGTAC 2160  
Db  
2101 CCAGCTGTCTGTAGTATATGATCGAGCATGTTGCGAACAAATGTTACTCTACACTGTAC 2160  
Qy  
2161 CATTTCACTGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTGAGTTT 2220  
Db  
2161 CATTTCACTGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTGAGTTT 2220  
Qy  
2221 ATGATTTATTTGGGTTTCAAAAGAGCTTCAATGACATTTAAATTTCTCTATAAGCATCT 2280  
Db  
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Qy  
2281 GCTACCCATCATATGATCAACAAAGCAAAACACACTCTCTCCATTTGCGGATATGTCAG 2340  
Db  
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Qy  
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Db  
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Qy  
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Db  
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Qy  
2461 AGTGATAGCGCTGTTTATAGTCCGATTCATCTCATACATCTGAGTCTTTTCTTTT 2520  
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Qy	2581	TGGGTGCAGGATACCATAACCATACACCATACACATACAGCATAACTATGGTCATTATA	2640
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Qy	2641	CCATATGGATGGACTGCATGTTTGGCTCTCTTATGGTTCCTTTAGCAGAAAAAGACAGTT	2700
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Qy	2701	TCAAGGAGAAAGAAAGCTGAGATGTTCAATGCTCACATGATTCTTCTATATGTTGCTCT	2760
Db	2701	TCAAGGAGAAAGAAAGCTGAGATGTTCAATGCTCACATGATTCTTCTATATGTTGCTCT	2760
Qy	2761	TCTCGTGACTCTTATTAAAAACCTTTCTAAATCACTTTGGTGGAAATTAACACATGACTGCA	2820
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Db	2821	TAAATTTGATGCAAGTTTTCAGACTTTTATTTGCTAAAAAATCTCTGATGATTATTAAACCTCA	2880
Qy	2881	ATTATATAAATTGCTGGATGAAGAGTTCAAAATTTGGACTAAATCTG	2925
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## RESULT 2

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US-10-736-318-22
; Sequence 22, Application US/10736318
; Publication No. US20040133948A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/10/736,318
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US/09/775,879
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Genomic HDF7
US-10-736-318-22

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Qy	241	AGTAA	CAGAAAGGCTAGAAATTATATAAATGTCAGCTGCACTTACTTTCACATATGTCAGAG	300
Db	241	AGTAA	CAGAAAGGCTAGAAATTATATAAATGTCAGCTGCACTTACTTTCACATATGTCAGAG	300
Qy	301	AGACTTCTGACTTAA	CCAGAGTTTGTAGATCTTTGTGTTTCTCTCTGCTCGAGCTGATT	360
Db	301	AGACTTCTGACTTAA	CCAGAGTTTGTAGATCTTTGTGTTTCTCTCTGCTCGAGCTGATT	360
Qy	361	GGAAATGA	CGAGAGTTCTTTTATCTACTTCCCTGGAGTGTAICTTGGTTAATCCAAAGGA	420
Db	361	GGAAATGA	CGAGAGTTCTTTTATCTACTTCCCTGGAGTGATCTTGGTTAATCCAAAGGA	420
Qy	421	TGTGACATCTAA	ATATTTACTTGTAACTTCTCTTACGTTTGTGTACAGGGCTGTCATTCA	480
Db	421	TGTGACATCTAAA	ATATTTACTTGTAACTTCTTACGTTTGTGTGTACAGGGCTGTCATTCA	480
Qy	481	CCCAGTAGACGGGATC	TTAAGGCTGTACCGCATGTGATAGCGCTGTTATAGTGCCTCAATT	540
Db	481	CCCAGTAGACGGGATC	TTAAGGCTGTACCGCATGTGATAGCGCTGTTATAGTGCCTCAATT	540
Qy	541	CATTTCACAA	CTCATATAGTCTTTTGTTCATGGAAGCGATATGGACGGCGAAATCCAT	600
Db	541	CATTTCACAACT	CTATATAGTCTTTTGTTCATGGAAGCGATATGGACGGCGAAATCCAT	600
Qy	601	GACTGCATCCAT	GGCAACATCTGGCCAGTAAATGGGTGCAGGATACCATGATACACAC	660
Db	601	GACTGCATCCAT	GGCAACATCTGGCCAGTAAATGGGTGCAGGATACCATGATACACAC	660
Qy	661	ACGACATACAAGCAT	AACTACTGTGCTATTATACCATATGGATGGATTCGATGTTTGGTCT	720
Db	661	ACGACATACAAGCAT	AACTACTGTGCTATTATACCATATGGATGGATTCGATGTTTGGTCT	720
Qy	721	CTTAGGGATCCT	CTCTTTAGAAGAGATGACAAACAAGACAGCTTCAAAGAAGCAGAGTGA	780
Db	721	CTTAGGGATCCT	CTCTTTAGAAGAGATGACAAACAAGACAGCTTCAAAGAAGCAGAGTGA	780
Qy	781	GAATGCCACCT	TGGGTTTGGTCTTCTGTTTTGTCTGTGTTGTGTTGTTCAAAGTTTC	840
Db	781	GAATGCCACCT	TGGGTTTGGTCTTCTGTTTTGTCTGTGTTGTGTTGTTCAAAGTTTC	840
Qy	841	AGCCTTCTCTGTTCT	TTTCTCTCTTTATTCATGTCCTCTCAACCTTTCCAAT	900
Db	841	AGCCTTCTCTGTTCT	TTTCTCTCTTTATTCATGTCCTCTCAACCTTTCCAAT	900
Qy	901	TATATTGTTACAA	CATTTCGTCTAGTTTAAAAACATGTAATGTTTGATGATCTTTGC	960
Db	901	TATATTGTTACAA	CATTTCGTCTAGTTTAAAAACATGTAATGTTTGATGATCTTTGC	960
Qy	961	AAGACTCCATTTT	TGTTTAAAGTAAAGCTTGAATCTCATAGATGTCGATGTTGGTATT	1020
Db	961	AAGACTCCATTTT	TGTTTAAAGTAAAGCTTGAATCTCATAGATGTCGATGTTGGTATT	1020
Qy	1021	TCCATTTTCAAGT	ACGGTTCTGTAGACGTGTAGTCTTGTCTGACCAAGTCCGGCTTAACACC	1080
Db	1021	TCCATTTTCAAGT	ACGGTTCTGTAGACGTGTAGTCTTGTCTGACCAAGTCCGGCTTAACACC	1080
Qy	1081	CCAAATTTCAA	AGNCTCACCAATCAAAATGCTGGCTGGCCCCCAATATATAGATGGGCCA	1140
Db	1081	CCAAATTTCAA	AGNCTCACCAATCAAAATGCTGGCTGGCCCCCAATATATAGATGGGCCA	1140
Qy	1141	GTTAATCCGTC	TAGCTTTTACCTTAAGCTTTAATCGTATTCAAAGAAAGACCCAGAGACTT	1200
Db	1141	GTTAATCCGTC	TAGCTTTTACCTTAAGCTTTAATCGTATTCAAAGAAAGACCCAGAGACTT	1200
Qy	1201	ATGAGTTTCC	TTTTTCTGTTTCAGCAGTTTACCTGTGTTACTTGAGAGTTGAGTTAATGG	1260
Db	1201	ATGAGTTTCC	TTTTTCTGTTTCAGCAGTTTACCTGTGTTACTTGAGAGTTGAGTTAATGG	1260
Qy	1261	TAGTAAACGCA	ATTTAAACCTTTAAGCTTTAATCGTATTCAAAGAAAGACCCAGAGACTT	1320
Db	1261	TAGTAAACGCA	ATTTAAACCTTTAAGCTTTAATCGTATTCAAAGAAAGACCCAGAGACTT	1320
Qy	1321	TAAATAAATCC	ATCGTAACCCCTCCACTTCAAAATCTTTTTTAAAAAGTAGCAATCAATT	1380

1321 TAAATAAATCCATCGTAACCTCCACTTCAAAATCTTTTAAAGTAGCAATCATTT 1380  
1381 AAATAATTGTAAGTTGCTTCAATCGAAAATTTGTAGTACAGATCTCAAAGCTCCTCGTTT 1440  
1381 AAATAATTGTAAGTTGCTTCAATCGAAAATTTGTAGTACAGATCTCAAAGCTCCTCGTTT 1440  
1441 GGCCATATCTCTCTAAACAAAGCATAGTAACACATTTGACCAAGTTGACCTCTCGGG 1500  
1441 GGCCATATCTCTCTAAACAAAGCATAGTAACACATTTGACCAAGTTGACCTCTCGGG 1500  
1501 GTTTTCATGGCGGCACTATGGCAGATTTAATGATCAGATCGTCAATGAGACCTCTTTT 1560  
1501 GTTTTCATGGCGGCACTATGGCAGATTTAATGATCAGATCGTCAATGAGACCTCTTTT 1560  
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1621 TCCTCCAGACATGGCTCCGGAATCTACCTGCGGGAACATACCTCTCTCTCTCTCTCT 1680  
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1801 GCCTGATAGATGTTGTTTACGTTTAACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860  
1861 TTCTACTCTCTCAATTAATAGTTTAAAGTTTAAATATTTTGGCTAATCCACATTTTATA 1920  
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1921 AGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTTGTTGGTTC 1980  
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1981 TTAGTTCTATTTCTGCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2040  
1981 TTAGTTCTATTTCTGCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2040  
2041 AAGGCAATGCTTTTGCAAAATATACGTTGCAATGAGGCTATGCTTGGTACACTCTTCTT 2100  
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2101 CAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCAATGTTACTCTACACTTGAC 2160  
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2161 CATTTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTAGTTT 2220  
2161 CATTTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTATCTGTTTGTAGTTAGTTT 2220  
2221 ATGATTTATTTGGGTTTCAAAAGGCTTCTGACATTTAAATTTCTCTATAAGCATCTCCAT 2280  
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2281 GCTACCCATCATATGATGACAAAGCAACACACTCTCTCCATTTGCGGTATGTCAAAG 2340  
2281 GCTACCCATCATATGATGACAAAGCAACACACTCTCTCCATTTGCGGTATGTCAAAG 2340  
2341 CTATATGTTCTCAATCTTAAATTTCAAGGCTTGTATCAATGAGTCTTCTTCTTCTTCTTCT 2400  
2341 CTATATGTTCTCAATCTTAAATTTCAAGGCTTGTATCAATGAGTCTTCTTCTTCTTCTTCT 2400  
2401 TTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGGATATCTTCAGGCTTATACCGC 2460

2401 TTTTCGGGTTTTTCAGGCTCGCATTCCTCCGCTGGACGGGATATCTTCAGGCTTATACCGC 2460  
2461 AGCTGATAGCGCTGTTTATAGTGGCGATTCATCTCATACACATCTGAGCTCTTTCTTTT 2520  
2461 AGCTGATAGCGCTGTTTATAGTGGCGATTCATCTCATACACATCTGAGCTCTTTCTTTT 2520  
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2641 CCAATATGATGAGTGGATGTTTGGCTCTCTTATGTTTCTTTAGCAGAAAAGACAGTT 2700  
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2701 TCAAGGAGAAAGAAAAGTGAGAAATGTTCAATGCTCACAATGATTTCTTCAATATGTTCTCT 2760  
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2881 ATTATATTAATTTGCTGATGAGAGTTCAAATTTGGACTAAATCTG 2925  
2881 ATTATATTAATTTGCTGATGAGAGTTCAAATTTGGACTAAATCTG 2925

## RESULT 3

US-09-775-879-20  
; Sequence 20, Application US/09775879  
; Patent No. US20020068822A1  
; GENERAL INFORMATION:  
; APPLICANT: Choe, Sunghwa  
; APPLICANT: Feldmann, Kenneth A  
; TITLE OF INVENTION: Dwf7 MUTANTS  
; FILE REFERENCE: 2225-0003  
; CURRENT APPLICATION NUMBER: US/09/775,879  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/179,901  
; PRIOR FILING DATE: 2000-02-02  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1889  
; TYPE: DNA  
; ORGANISM: Genomic dwf7 (Arabidopsis)  
US-09-775-879-20

Query Match 31.6%; Score 924.4; DB 3; Length 1889;  
Best Local Similarity 99.6%; Pred. No. 5.6e-204;  
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;  
QY 1 GTTTGGTATTTATTTGGATGACAGAGCTTCAATGACATTAAGCCCTCTCTATAAGTATCT 60  
DB 929 GTTTGGTATTTATTTGGATGACAGAGCTTCAATGACATTAAGCCCTCTCTATAAGTATCT 988  
QY 61 CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGTAAAGTG 120  
DB 989 CCATGCCACCCATCATATCTCAACAAGCAGAAATACATCTCTCCATTTGCCGGTAAAGTG 1048  
QY 121 TTTTCAGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180  
DB 1049 TTTTCAGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1108  
QY 181 AAAAGACTTTTGTGACGAGCTGCTGTACTCTCAAAATCAATTTTGCATTTCTTATCCATAA 240

Db	1109	AAAAAGACTTTGTTCAGCAGCTGCTTGTACTCCAAATCACTTTTGCAATTCCTTATCCATAA	1168
Qy	241	AGTAACCAAGAAAGGCTAGAAATTATATAAATGTTCAGCTGCATTACTTCACATATGTCTCAGAG	300
Db	1169	AGTAACCAAGAAAGGCTAGAAATTATATAAATGTTCAGCTGCATTACTTCACATATGTCTCAGAG	1228
Qy	301	AGACTTCTGACTTAACCAAGAGTTAGATCTTTGTGTTTCTCTCTGCTGCTCGGACTGATT	360
Db	1229	AGACTTCTGACTTAACCAAGAGTTAGATCTTTGTGTTTCTCTCTGCTGCTCGGACTGATT	1288
Qy	361	GGAAATGACGAGAAGTTCTTTTATCTACTCTCCCTGGAGTGTAATCTTGGTTAAATCCAAAGGA	420
Db	1289	GGAAATGACGAGAAGTTCTTTTATCTACTCTCCCTGGAGTGTAATCTTGGTTAAATCCAAAGGA	1348
Qy	421	TGTGACATCTAAATATTAATCTTGTAACTTCCTTACGTTTCTTTGTTTTCACAGGCGCTTGCA--TTC	479
Db	1349	TGTGACATCT--AAATATTAATCTTGTAACTTCCTTACGTTTCTTTGTTTTCACAGGCGCTTGCAATTC	1407
Qy	480	ACCAGTAGACGGGATACTTAAAGGCTGTACCGCATGTGATAGCGCTG--TTATAGTGCCTAA	538
Db	1408	ACCAGTAGACGGGATACTTCAGGCTGTACCGCATGTGATAGCGCTGTTTATAGTGCCTAA	1467
Qy	539	TTCAATTTCAAACTCAATATAGGTCTTTTGTTCATGGAAGCATATGACCGCGCAACATCC	598
Db	1468	TTCAATTTCAAACTCATATAGGTCTTTTGTTCATGGAAGCATATGACCGCGCAACATCC	1527
Qy	599	ATGACTGCATCCATGGCAACATCTGGCGCAGTAATGGGTGCAGGATACCATACGATACACC	658
Db	1528	ATGACTGCATCCATGGCAACATCTGGCGCAGTAATGGGTGCAGGATACCATACGATACACC	1587
Qy	659	ACACGACATACAAGCATAACTATTCGTCAATTATACCATATGCATGCGATTGCGATGTTTGGCT	718
Db	1588	ACACGACATACAAGCATAACTATTCGTCAATTATACCATATGCATGCGATTGCGATGTTTGGCT	1647
Qy	719	CTCTTAGGGATCCTCTCTTAGAAGAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGT	778
Db	1648	CTCTTAGGGATCCTCTCTTAGAAGAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGT	1707
Qy	779	GAGAAATGCCCACTTGGGTTTTGTTCTTCTGTTTGTCTGTGTTGTTGTTGTTGTTTCAAAAGTT	838
Db	1708	GAGAAATGCCCACTTGGGTTTTGTTCTTCTGTTTGTCTGTGTTGTTGTTGTTGTTTCAAAAGTT	1767
Qy	839	TCAGCCTTCTGTGTTCTTTTCTCTCTCTCTCTTATTCATGNGTCTCTCTCAACCTTTCCA	898
Db	1768	TCAGCCTTCTGTGTTCTTTTCTCTCTCTCTCTTATTCATGNGTCTCTCTCAACCTTTCCA	1827
Qy	899	ATTATATTGTTTACAAACATTTGCTGCTAGTTTAAAAACATGTAATGTTTGAATGATCTTT	958
Db	1828	ATTATATTGTTTACAAACATTTGCTGCTAGTTTAAAAACATGTAATGTTTGAATGATCTTT	1887
Qy	959	GC 960	
Db	1888	GC 1889	

## RESULT 4

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US-10-736-318-20
; Sequence 20, Application US/10736318
; Publication No. US20040133948A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A
; TITLE OF INVENTION: Dwf7 MUTANTS
; FILE REFERENCE: 2225-0003
; CURRENT APPLICATION NUMBER: US/10/736,318
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US/09/775,879
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,901
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0

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; SEQ ID NO 20
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Genomic dwf7 (Arabidopsis)
US-10-736-318-20

Query Match      31.6%; Score 924.4; DB 7; Length 1889;
Best Local Similarity 99.6%; Pred. No. 5.6e-204;
Matches 958; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 1 GTTTGGTATTATTGGATGCACAGAGGCTTCATGACATTAAGCCTCTCTATAGTATCT 60
DB 929 GTTTGGTATTATTGGATGCACAGAGGCTTCATGACATTAAGCCTCTCTATAGTATCT 988

QY 61 CCATGCCACCACCATCATATCTTACAAACAGAGAGATACACTCTCTCCATTTGCCGGTAAAGTG 120
DB 989 CCATGCCACCACCATCATATCTTACAAACAGAGAGATACACTCTCTCCATTTGCCGGTAAAGTG 1048

QY 121 TTTTTCAGTTTGGTCTCTTTTAGTCTTGTTGTAAGATGTTGGTAGCAATTTAGTFTTCTTACCAG 180
DB 1049 TTTTTCAGTTTGGTCTCTTTTAGTCTTGTTGTAAGATGTTGGTAGCAATTTAGTFTTCTTACCAG 1108

QY 181 AAAAGACTTTGTTCAGCAGCTGCTTGTTACTTCCAATCACATTTTTCATCTCTTATCCATAA 240
DB 1109 AAAAGACTTTGTTCAGCAGCTGCTTGTTACTTCCAATCACATTTTTCATCTCTTATCCATAA 1168

QY 241 AGTAAACAGAAAGGCTAGAAATATATAAATGTTCAGCTGCAATTAATCTTACATATGTTCAGAG 300
DB 1169 AGTAAACAGAAAGGCTAGAAATATATAAATGTTCAGCTGCAATTAATCTTACATATGTTCAGAG 1228

QY 301 AGACTTCTGACTTAAACCCAGAGTTTAGATCTTTGTGTTTCTCTTCGTCTCGGACTGATTT 360
DB 1229 AGACTTCTGACTTAAACCCAGAGTTTAGATCTTTGTGTTTCTCTTCGTCTCGGACTGATTT 1288

QY 361 GGAATTCAGCAGAGAGTCTTTTATCTACTTCCCTCGAGGTGATCTTGGTTAAATCCCAAGGA 420
DB 1289 GGAATTCAGCAGAGAGTCTTTTATCTACTTCCCTCGAGGTGATCTTGGTTAAATCCCAAGGA 1348

QY 421 TGTGACATCTTAAATATTTACTTTGTAACCTTCCTTACGTTTGTGTTTACAGGCTTTGCA -TTC 479
DB 1349 TGTGACATCT -AATATATCTTGTAACTTTCCTTACGTTTGTGTTTACAGGCTTTGCA-TTTC 1407

QY 480 ACCCAGTACGCGGATACCTTAAAGGCTGTACCGCATGTGATAGCGCTG -TTATAGTGCCAA 538
DB 1408 ACCCAGTACGCGGATACCTTACGSGCTGTACCGCATGTGATAGCGCTGTTTATAGTGCCAA 1467

QY 539 TTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCATATGCA CGCGCAACATCC 598
DB 1468 TTCATTTCAAACTCATATAGGTCCTTTTGTTCATGGAAGCATATGCA CGCGCAACATCC 1527

QY 599 ATGACTGCATCCATGSCAACATCTGCGCAGTAATGGTGCAGGATACCATACCATACACC 658
DB 1528 ATGACTGCATCCATGSCAACATCTGCGCAGTAATGGTGCAGGATACCATACCATACACC 1587

QY 659 ACACGACATCAACAGCATAACTATGGTCAATTATACCATATGGATGGATTTGGATGTTTGGCT 718
DB 1588 ACACGACATCAACAGCATAACTATGGTCAATTATACCATATGGATGGATTTGGATGTTTGGCT 1647

QY 719 CTCTTAGGGATCTCTCTTAGAAGAAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGT 778
DB 1648 CTCTTAGGGATCTCTCTTAGAAGAAAGATGACAAACAAAGACAGCTTCAAGAAAGCAGAGT 1707

QY 779 GAGAAATGCCACATTTGGGTTTGTCTCTGTTTGTGCTTGTGTTGTGTTGTTGTTCAAGTT 838
DB 1708 GAGAAATGCCACATTTGGGTTTGTCTCTGTTTGTGCTTGTGTTGTGTTGTTGTTCAAGTT 1767

QY 839 TCAGCCTTTCTTGTCTTTTCTTCTTCTTATTCATGTGCTCTCTCAACCTTTCCA 898
DB 1768 TCAGCCTTTCTTGTCTTTTCTTCTTCTTATTCATGTGCTCTCTCAACCTTTCCA 1827

QY 899 ATTATATGTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTGTTGATGATCTTT 958
DB 1828 ATTATATGTGTACAAACATTTGCTGTCTAGTTTAAACATGTAAATGTGTTGATGATCTTT 1887

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QY 959 GC 960  
Db 1888 GC 1889

RESULT 5

US-09-885-723-23  
; Sequence 23, Application US/09885723  
; Publication No. US20030150008A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS  
; FILE REFERENCE: MTC6783.1  
; CURRENT APPLICATION NUMBER: US/09/885,723  
; CURRENT FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 1175  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-885-723-23

Query Match 15.8%; Score 461; DB 3; Length 1175;  
Best Local Similarity 97.6%; Pred. No. 2.3e-96;  
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
  
QY 462 TTTACAGGCGTTGCA-TTCACCCAGTAGCGGATCTTAAGCTCTACCGCATGTGATA 520  
Db 643 TTTGCCGGCGTTGCAATTCACCCAGTAGCGGATCTTCAGGCTGTACCGCATGTGATA 702  
  
QY 521 GCGCTG-TTATAGTGCATTTTCACAACTCATATAGTCTTTTGTTCATGGAGCG 579  
Db 703 GCGCTGTTTATAGTGCCAAATTCATTCACAACTCATATAGTCTTTTGTTCATGGAGCG 762  
  
QY 580 ATATGACGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639  
Db 763 ATATGGCGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822  
  
QY 640 GGATACCATACGATACACACAGCATACAAGCATTAATGGTCAATTAACCATATGG 699  
Db 823 GGATACCATACGATACACACAGCATACAAGCATTAATGGTCAATTAACCATATGG 882  
  
QY 700 ATGGATGGATGTTGGCTCTCTTAGGGATCCCTCTTAGAAGAGATGACAAAGAC 759  
Db 883 ATGGATGGATGTTGGCTCTCTTAGGGATCCCTCTTAGAAGAGATGACAAAGAC 942  
  
QY 760 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACCTTGGGTTTGTCTCTCTTTTGTCTTGT 819  
Db 943 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACCTTGGGTTTGTCTCTCTTTTGTCTTGT 1002  
  
QY 820 GTTGTGTTGTTCAAAAGTTTCAGCCTTCTTGTCTCTTTCTCTTCTTCTTATTCATGT 879  
Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCTTCTTGTCTCTTTCTCTTCTTCTTATTCATGT 1062  
  
QY 880 GTCTCTCAACCTTCCAAATTAATTTACAAATTTGTTACAAATTTGCTCTAGTTTAAACATG 939  
Db 1063 GTCTCTCAACCTTCCAAATTAATTTACAAATTTGTTACAAATTTGCTCTAGTTTAAACATG 1122  
  
QY 940 TAAATGTTTGATCATCTTTGC 960  
Db 1123 TAAATGTTTGATCATCTTTCC 1143

RESULT 6

US-10-862-907-23  
; Sequence 23, Application US/10862907  
; Publication No. US20050086713A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID COMPOUNDS  
; FILE REFERENCE: MTC6783.1

; CURRENT APPLICATION NUMBER: US/10/862,907  
; CURRENT FILING DATE: 2004-06-07  
; PRIOR APPLICATION NUMBER: US/09/885,723  
; PRIOR FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 1175  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-862-907-23

Query Match 15.8%; Score 461; DB 9; Length 1175;  
Best Local Similarity 97.6%; Pred. No. 2.3e-96;  
Matches 489; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
  
QY 462 TTTACAGGCGTTGCA-TTCACCCAGTAGCGGATCTTAAGCTCTACCGCATGTGATA 520  
Db 643 TTTGCCGGCGTTGCAATTCACCCAGTAGCGGATCTTCAGGCTGTACCGCATGTGATA 702  
  
QY 521 GCGCTG-TTATAGTGCATTTTCACAACTCATATAGTCTTTTGTTCATGGAGCG 579  
Db 703 GCGCTGTTTATAGTGCCAAATTCATTCACAACTCATATAGTCTTTTGTTCATGGAGCG 762  
  
QY 580 ATATGACGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 639  
Db 763 ATATGGCGCGCAACATCCATGACTGCATCCATGGCAACATCTGGCCAGTAATGGGTGCA 822  
  
QY 640 GGATACCATACGATACACACAGCATACAAGCATTAATGGTCAATTAACCATATGG 699  
Db 823 GGATACCATACGATACACACAGCATACAAGCATTAATGGTCAATTAACCATATGG 882  
  
QY 700 ATGGATGGATGTTGGCTCTCTTAGGGATCCCTCTTAGAAGAGATGACAAAGAC 759  
Db 883 ATGGATGGATGTTGGCTCTCTTAGGGATCCCTCTTAGAAGAGATGACAAAGAC 942  
  
QY 760 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACCTTGGGTTTGTCTCTCTTTTGTCTTGT 819  
Db 943 AGCTTCAAGAAAGCAGAGTGAGAAATGCCACCTTGGGTTTGTCTCTCTTTTGTCTTGT 1002  
  
QY 820 GTTGTGTTGTTCAAAAGTTTCAGCCTTCTTGTCTCTTTCTCTTCTTCTTATTCATGT 879  
Db 1003 GTTGTGTTGTTCAAAAGTTTCAGCCTTCTTGTCTCTTTCTCTTCTTCTTATTCATGT 1062  
  
QY 880 GTCTCTCAACCTTCCAAATTAATTTACAAATTTGTTACAAATTTGCTCTAGTTTAAACATG 939  
Db 1063 GTCTCTCAACCTTCCAAATTAATTTACAAATTTGTTACAAATTTGCTCTAGTTTAAACATG 1122  
  
QY 940 TAAATGTTTGATCATCTTTGC 960  
Db 1123 TAAATGTTTGATCATCTTTCC 1143

RESULT 7

US-09-938-842A-421  
; Sequence 421, Application US/09938842A  
; Patent No. US20030160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22



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; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 421
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-421

Query Match      11.9%; Score 347.2; DB 3; Length 846;
Best Local Similarity 72.4%; Pred. No. 5.7e-70;
Matches 508; Conservative 0; Mismatches 108; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGCAGATATAGTGGCAATGAAGCTAT 2081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 AGATGCAATTCCTACAAATGAAGCTATGCGTTTGCAAAATGTTGTGGCAATGAAGCTAT 284

QY 2082 GCCTTGGTACATCTCTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GCATGGAACATCTCTCTCCAACTGCTCCGAGAGTATGATGAACGTTGGTTGGACCA 344

QY 2142 ATGTTACTCTACACTTGACCAATTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTA 2201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ATGTTTGTCTAGCATAGGGAATTCGGCTGGATCTCTGTTTGTATCTACATGCCATCTA 404

QY 2202 TCTTGTCTTGTAGTTTATGATTTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TCTTGTCTTGTAGTTTATGATTTTATTTGGATGACAGAGAGCTTCATGACATTAAGCC 464

QY 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAGCAACACACTCTCTCC 2321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 TCTCTATAAGTATCTCCATGCGACCCCATCATATCTACAAAGCAAGCAATACACTCTCTCC 524

QY 2322 ATTTGCCGATATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 ATTTGCC----- 531

QY 2382 TGACTTCTTACTTGATGTTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGG 2441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 -----GGGCTTGCATTTTCAACCCAGTAGACGGG 558

QY 2442 ATACTTCAGGCTATACCGCATGATAGCGCTGTTTATAGTCCGATTCATCTCATACA 2501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 ATACTTCAGGCTGATACCGCATGATAGCGCTGTTTATAGTCCCAATTCATTTCAACT 618

QY 2502 CATCTGAGTCTTTTGTGTTTGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 CATATAGTCTTTTGTTCATGAGCGATATGACAGCGGAATCCATGACTGCATCCAT 678

QY 2562 GGTAAACATCTGGCCTATTAATGGGTGAGGATACCATACATACACCATACAACATACAAG 2621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 GGCAACATCTGGCCAGTAAATGGGTGAGGATACCATACATACACCATACAACATACAAG 738

QY 2622 CATTAATGCTCATTAACCATATGATGGAGTGGATGTTGGCTCTCTTATGTTCTCT 2681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 CATAACTATGGTCAATTAACCATATGATGGATGGATGTTGGCTCTCTTATGTTCTCT 798

QY 2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAGAAAGTGAAG 2723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 CTCTTAGAAGATGACAAACAGACAGCTTCAGAAAGCA 840

RESULT 8
US-09-938-842A-421
; Sequence 421, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 421
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-421

Query Match      11.9%; Score 347.2; DB 3; Length 846;
Best Local Similarity 72.4%; Pred. No. 5.7e-70;
Matches 508; Conservative 0; Mismatches 108; Indels 86; Gaps 1;

QY 2022 AGAATCCATCTCTACGAGAAAGCAATGCTTTTGCAGATATAGTGGCAATGAAGCTAT 2081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 AGATGCAATTCCTACAAATGAAGCTATGCGTTTGCAAAATGTTGTGGCAATGAAGCTAT 284

QY 2082 GCCTTGGTACATCTCTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GCATGGAACATCTCTCTCCAACTGCTCCGAGAGTATGATGAACGTTGGTTGGACCA 344

QY 2142 ATGTTACTCTACACTTGACCAATTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTA 2201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 ATGTTTGTCTAGCATAGGGAATTCGGCTGGATCTCTGTTTGTATCTACATGCCATCTA 404

QY 2202 TCTTGTCTTGTAGTTTATGATTTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TCTTGTCTTGTAGTTTATGATTTTATTTGGATGACAGAGAGCTTCATGACATTAAGCC 464

QY 2262 TCTCTATAAGCATCTCCATGCTACCCATCATATGTACAAAGCAAGCAACACACTCTCTCC 2321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 TCTCTATAAGTATCTCCATGCGACCCCATCATATCTACAAAGCAAGCAATACACTCTCTCC 524

QY 2322 ATTTGCCGATATGTCAAAGCTATATGTTCTCAATCTAAATTCAGAGCTTGTATCAATGG 2381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 ATTTGCC----- 531

QY 2382 TGACTTCTTACTTGATGTTTTTTCGGGTTTTTCAGGCTCGCATTCATCCGCTGGACGGG 2441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 -----GGGCTTGCATTTTCAACCCAGTAGACGGG 558

QY 2442 ATACTTCAGGCTATACCGCATGATAGCGCTGTTTATAGTCCGATTCATCTCATACA 2501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 ATACTTCAGGCTGATACCGCATGATAGCGCTGTTTATAGTCCCAATTCATTTCAACT 618

QY 2502 CATCTGAGTCTTTTGTGTTTGAAGGATATGACAGCAAGCATCCATGATTCATACAT 2561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 CATATAGTCTTTTGTTCATGAGCGATATGACAGCGGAATCCATGACTGCATCCAT 678

QY 2562 GGTAAACATCTGGCCTATTAATGGGTGAGGATACCATACATACACCATACAACATACAAG 2621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 GGCAACATCTGGCCAGTAAATGGGTGAGGATACCATACATACACCATACAACATACAAG 738

QY 2622 CATTAATGCTCATTAACCATATGATGGAGTGGATGTTGGCTCTCTTATGTTCTCT 2681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 CATAACTATGGTCAATTAACCATATGATGGATGGATGTTGGCTCTCTTATGTTCTCT 798

QY 2682 TTAGCAGAAAAGACAGTTTCAAGGAGAAAGAAAGTGAAG 2723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 CTCTTAGAAGATGACAAACAGACAGCTTCAGAAAGCA 840

RESULT 9
US-10-224-880C-27
; Sequence 27, Application US/10224880C
; Publication No. US20030229914A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
```



; APPLICANT: Orozco, Emil M.  
; APPLICANT: Rafaleki, J. Antoni  
; APPLICANT: Shen, Jennie B.  
; TITLE OF INVENTION: Sterol Metabolism Enzymes  
; FILE REFERENCE: BB1282 US DIV  
; CURRENT APPLICATION NUMBER: US/10/224,880C  
; CURRENT FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: 60/109,283  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 27  
; LENGTH: 1447  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-224-880C-27

Query Match 7.0%; Score 203.4; DB 6; Length 1447;  
Best Local Similarity 61.3%; Pred. No. 2e-36;  
Matches 399; Conservative 0; Mismatches 166; Indels 86; Gaps 1;  
QY 2022 AGAATCCATCTTACGAGAAAGCAATGCTTTTGCATAATATACGTGGCAATGAGGCTAT 2081  
|||  
Db 316 AGATGCTATTCCCTCTCAAAGAGCCATGCTCTTGCATAATATCTGTGCTATGAAGCCAT 375  
|||  
QY 2082 GCCTTGGTACACTCTTCCAGCTCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141  
|||  
Db 376 GCCGTGGTACTCTTACTTCCAACTGTTTCGGAGTACCTGGTAGAACTGGCTGGCAAA 435  
|||  
QY 2142 ATGTACTCTACACTTTCACCATTTCAACTGGTTCTCTGTTTCTCTACATAGCTCTCTA 2201  
|||  
Db 436 GTGCTATCTAGATTATATATGTTGGTTGGCTGTCATCTGTTGATTAGCAATTTA 495  
|||  
QY 2202 TCTTGTGTTTGTAGTTTGAATTAATGTTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261  
|||  
Db 496 TCTAAATTATGTAGAGTTTGGTATTTATTTGGATGTCACAGAGCTGCGACATAAAACC 555  
|||  
QY 2262 TCTCTATAGCATCTCCATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCC 2321  
|||  
Db 556 GCCTTACAAATATCTTCATGCTACCCATCATCTACAAATAAAGAACACTCTCTCCCC 615  
|||  
QY 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381  
|||  
Db 616 TTTTGTGTTTG 628  
|||  
QY 2382 TGACTTCTTTACTTGATGTTTTCGGGTTTTCAGGCTGCGCATTCATCCGCTGGAGCGG 2441  
|||  
Db 629 -----GCATTTCAACCCTCTTGATGG 649  
|||  
QY 2442 ATACTTCAGGCTATACGCAAGTGATAGCGCTGTTTATAGTCCGATTCTATCTCATAACA 2501  
|||  
Db 650 ATACTTCAGGCTATACGCAAGTGATAGCGCTGTTTATAGTCCGATTCTATCTCATAACA 709  
|||  
QY 2502 CATCTGAGTCTTTGTTTGGAGGATGATGACAGCAAGCATCCATGATTCATACAT 2561  
|||  
Db 710 CATTTGGCCCTCATATTCATTTAGGGGTTTGACTGCAATATTCATGATTGATTCAT 769  
|||  
QY 2562 GGTAAACATCTGGCTATATGTTGGTGGAGGATACCATCAACATACCATCAACATCAAG 2621  
|||  
Db 770 GGAATAATGTTGGCTGTTATGGGTGCTGTTTACCAACACCATTCATCACATACATACGG 829  
|||  
QY 2622 CATAACTATGGTCAATATACCATATGATGGAGCTGGATGTTTGGCTCTCT 2672  
|||  
Db 830 CACAACCTACGGCCACTACACCATATGATGGATTGGATGTTTGGAACTCTT 880  
|||

RESULT 10  
US-10-767-701-13122  
; Sequence 13122, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 13122  
; LENGTH: 1253  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS11413\_1  
US-10-767-701-13122

Query Match 6.9%; Score 200.8; DB 7; Length 1253;  
Best Local Similarity 61.1%; Pred. No. 7.6e-36;  
Matches 397; Conservative 0; Mismatches 167; Indels 86; Gaps 1;  
QY 2022 AGAATCCATCTTCTACGAGAAAGCAATGCTTTTGCATAATATACGTGGCAATGAGGCTAT 2081  
|||  
Db 308 AGATGCCATTTCCCAAAATGAAGCTATGAAGAAGCAATAGTTGTAGCATCGAGGCTAT 367  
|||  
QY 2082 GCCTTGGTACACTCTTCTTCCAGCTGTCTCTGAGTATATGATCGAGCATGGTTGGACCA 2141  
|||  
Db 368 GCCTTTTACTGCTCTCTTCCAACTTTATCTGAATATATGATTGAGAGCGGATGGACCCA 427  
|||  
QY 2142 ATGTTACTCTACACTTGACCATTTCAACTGGTTCTCTGTTTCTCTCTACATAGCTCTCTA 2201  
|||  
Db 428 GTGTTACTTTAATATCAGTGAAGTTGGTTTTTCTATGTACCTCTGTATATGGCTATGA 487  
|||  
QY 2202 TCTGTTTTTGTAGTTTATGATTTATGGGTTTCAAAAGAGCTTCATGACATTAAT 2261  
|||  
Db 488 TCTCAATTTTGTGGATTGGAAATTTACTGGATGACAGAGATTGTCATGACATAAAGCC 547  
|||  
QY 2262 TCTCTATAGCATCTCCATGCTACCCATCATATGTACAAAGCAAAACACACTCTCTCC 2321  
|||  
Db 548 ATTATACAAATATCTGCATGCAACCCATCATATTTACAAAGGAAATACTTTGTCTCC 607  
|||  
QY 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381  
|||  
Db 608 ATTTG----- 612  
|||  
QY 2382 TGACTTCTTTACTTGATGTTTTCGGGTTTTCAGGCTGCGCATTCATCCGCTGGAGCGG 2441  
|||  
Db 613 -----CTGGACTTGCATTTTCATCCACTGGATGGT 641  
|||  
QY 2442 ATACTTCAGGCTATACGCAAGTGATAGCGCTGTTTATAGTCCGATTCTATCTCATAACA 2501  
|||  
Db 642 ATTTGCAAGCAATACCAATGTTTGGCTCTTCTCTTTTCCAACTCACTTCAGGACA 701  
|||  
QY 2502 CATCTGAGTCTTTGTTTGGAGGATATGAGCAGCAGCATCCATGATTCATATCATATCAT 2561  
|||  
Db 702 CATATGCTCTCTGTTCTTAGAGCGCTGTGAGCAACAAACATCCACGACTGCTCAT 761  
|||  
QY 2562 GGTAAACATCTGGCTATATGTTGGTGGAGTACCATACCATACCAACATCAACATCAAG 2621  
|||  
Db 762 GGCAGATATGGCAGTCAATGGCGCTGGATATCACCAATTCACCATACACTTACACTTACCGC 821  
|||  
QY 2622 CATAACTATGGTCAATATACCATATGATGGAGCTGGATGTTTGGCTCTCT 2671  
|||  
Db 822 CACAACCTATGGCCACTACACCATCTGGATGGAGCTGGATGTTTAGTACCCT 871  
|||

RESULT 11  
US-10-259-194A-287  
; Sequence 287, Application US/10259194A  
; Publication No. US20040010815A1  
; GENERAL INFORMATION:  
; APPLICANT: Lange, Markus B.  
; APPLICANT: Ghasseman, Majid  
; APPLICANT: Briggs, Steven P.  
; APPLICANT: Cooper, Bret

```

Qy      2683 TAG 2685
Db      ||
      811 AAG 813

RESULT 12
US-10-259-194A-530
; Sequence 530, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassemanian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, FumiYaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricks, Barrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 530
; LENGTH: 1135
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-259-194A-530

Query Match      6.4%; Score 188; DB 6; Length 1135;
Best Local Similarity 59.8%; Pred. No. 6.8e-33;
Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

Qy      2022 AGAATCCATTCTTCACGAGAAAGGCAATGCTTTTGCAAATATAGCTGTGCAATAGAGGCTAT 2081
Db      |||||
      220 AGATGCTGTCCTACAGTATGAGAGCAATATATGTTGCATCAAGGCTAT 279

Qy      2082 GCCTGGTACACTCTCTCTTCACGCTGTCTCTGAGTATATGATGACGATGGTTGGACCAA 2141
Db      |||||
      280 GCCTTTCTACTGTGCTCTTCCGTCGCTATCTGAGCACATGATTTGAGAGTGGATGGACACG 339

Qy      2142 ATGTCTACTCTACACTTTCACCATTTCAACTGGTTCCCTGTTCTCTCTACATAGCTCTCTA 2201
Db      |||||
      340 GUGTTTCTTTCATATCAGCGAGTTGGTTGGCCCTATGTACATTTCTATGTGTCCTCTATA 399

Qy      2202 TCTGTTTTAGTTGAGTTTATGATTTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2261
Db      |||||
      400 TCTCATCTTTGTGGAGTTTCGGAATTTACTGGATGTCACAGAGTTGTCATGACATATAAGCC 459

Qy      2262 TCTCTATAGCATCTCCATGCTACCCCATCATATGTATGACAAAGCAAAACACACTCTCTCC 2321
Db      |||||
      460 ACTATACAAGACCTCATATGCAACCCACCACATTTTACAACAGGAGTAACCCCTATCACC 519

Qy      2322 ATTTGCCGGTATGTCAAAGCTATATGTTCTCAATTAATTTCAAGAGCTTTGTATCAATGG 2381
Db      |||||
      520 ATTTG-----
      524

Qy      2382 TGACTTCTTACTTGATGTTTTTCGGGTTTTTCAGGGCTCGCATTCATCCATCGCTGGACGG 2441
Db      |||||
      525 -----CTGGACTAGCATTTCCATTCATTTGGACGG 553

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QY 2442 ATACTTCAGGCTATACCGCAGCTGATAGCGCTGTTTATAGTGCAGATTTCATCTCAATAACA 2501  
|||||  
Db 554 ATACTCGAAGCCATATCGCAGCTGATGCTCTGTTCTCTCCGATGCACTTCAGGACG 613  
|||||  
QY 2502 CATCTGAGTCTTTTGGTGGTGGATATGACACAGCAAGCATCCATGATTGCATACAT 2561  
|||||  
Db 614 CACATTGCTCTCTATTATAGAGCGGTTGGAGCGCAAAATCCACGACTGCATCCAC 673  
|||||  
QY 2562 GGTAAATCTGGCCTTAATATGGTGGAGGATACCATACCATACATCAACATCAACAAG 2621  
|||||  
Db 674 GGAAGATCTGGCCGGTGTATGGCGCGGTACACACCATCCACACAGCAGTACCGG 733  
|||||  
QY 2622 CATAACTATGCTCATATACCATATGATGATGGAGCTGGATGTTGGCTCTCT 2671  
|||||  
Db 734 CACAACATATGGCCACTACACCGTGTGATGGAGTGGCTGTTGGGCAACCT 783  
|||||

## RESULT 13

US-10-224-880C-29

; Sequence 29, Application US/10224880C

; Publication No. US20030229914A1

; GENERAL INFORMATION:

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Orozco, Emil M.

; APPLICANT: Rafaleki, J. Antoni

; APPLICANT: Shen, Jennie B.

; TITLE OF INVENTION: Sterol Metabolism Enzymes

; FILE REFERENCE: BB1282 US DIV

; CURRENT APPLICATION NUMBER: US/10/224,880C

; CURRENT FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: 60/109,283

; PRIOR FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 29

; LENGTH: 1210

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1130)

; OTHER INFORMATION: n = A, C, G, or T

US-10-224-880C-29

Query Match 6.4%; Score 188; DB 6; Length 1210;

Best Local Similarity 59.8%; Pred. No. 7e-33;

Matches 389; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

QY 2022 AGAATCCATTCTCTACGAGAAAGGCAATGCTTTTGCAAAATATACGTGGCAATGAAGGCTAT 2081  
|||||  
Db 188 AGATGCTGTCCTTACAGTAGAGCTATGAAGAGCAATATTTGTCATCAAGGCTAT 247  
|||||  
QY 2082 GCCTGGTACACTCTTCTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2141  
|||||  
Db 248 GCCTTTCTACTGTGCTCTCCGTCGCTATCTGAGCACATGATTGAGAGTGGATGGACAG 307  
|||||  
QY 2142 ATGTTACTTACACTTGACCAATTTCACTGGTTCCTGTTCTCTCTACATAGCTCTCTA 2201  
|||||  
Db 308 GTGTTTCTTTTCATATCAGCGAAGTTGGTTGGCCTATGTACATTTATCTATGTGCTCTATA 367  
|||||  
QY 2202 TCTGTTTTAGTTGAGTTATGATTTATTTGGTTTCAAAAGAGCTTCATGACATTAAT 2261  
|||||  
Db 368 TCTCATCTTTGAGGTTTCGGAATTTTACGTGATGCAAGAGTTGTCATGACATTAAGCC 427  
|||||  
QY 2262 TCTCTATAAGCACTCTCCATGCTACCCATCATATGTACAACAGCAAAACACACTCTCTCC 2321  
|||||  
Db 428 ACTATACAAGCACTTACATGCAACCCACCATTTTACACAAGGAGAAATACCCATATCAC 487  
|||||  
QY 2322 ATTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGG 2381  
|||||  
Db 488 ATTTG----- 492  
|||||  
QY 2382 TGACTCTTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCATTCATCCGCTGGACGGG 2441  
|||||

Db 493 -----CTGGACTAGCATTTCCATCCATTTGGACGGG 521  
|||||  
QY 2442 ATACTTCAGGCTATACCGCAGCTGATAGCGCTGTTTATAGTGCAGATTTCATCTCAATAACA 2501  
|||||  
Db 522 ATACTCGAAGCCATATCGCAGCTGATGCTCTGTTCTCTCCGATGCACTTCAGGACG 581  
|||||  
QY 2502 CATCTGAGTCTTTTGGTGGTGGATATGACACAGCAAGCATCCATGATTGCATACAT 2561  
|||||  
Db 582 CACATTGCTCTCTATTATAGAGCGGTTGGAGCGCAAAATCCACGACTGCATCCAC 641  
|||||  
QY 2562 GGTAAATCTGGCCTTAATATGGTGGAGGATACCATACCATACATCAACATCAACAAG 2621  
|||||  
Db 642 GGAAGATCTGGCCGGTGTATGGCGCGGTACACACCATCCACACAGCAGTACCGG 701  
|||||  
QY 2622 CATAACTATGCTCATATACCATATGATGATGGAGCTGGATGTTGGCTCTCT 2671  
|||||  
Db 702 CACAACATATGGCCACTACACCGTGTGATGGAGTGGCTGTTGGGCAACCT 751  
|||||

## RESULT 14

US-10-224-880C-23

; Sequence 23, Application US/10224880C

; Publication No. US20030229914A1

; GENERAL INFORMATION:

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Orozco, Emil M.

; APPLICANT: Rafaleki, J. Antoni

; APPLICANT: Shen, Jennie B.

; TITLE OF INVENTION: Sterol Metabolism Enzymes

; FILE REFERENCE: BB1282 US DIV

; CURRENT APPLICATION NUMBER: US/10/224,880C

; CURRENT FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: 60/109,283

; PRIOR FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 23

; LENGTH: 911

; TYPE: DNA

; ORGANISM: Zea mays

US-10-224-880C-23

Query Match 6.4%; Score 187; DB 6; Length 911;

Best Local Similarity 59.8%; Pred. No. 1e-32;

Matches 398; Conservative 0; Mismatches 175; Indels 86; Gaps 1;

QY 2023 GAATCCATTCTCTACGAGAAAGGCAATGCTTTTGCAAAATATACGTGGCAATGAAGGCTATG 2082  
|||||  
Db 74 GATGCCATCCCCACAAATGAAGCTATGAAGAGCAAAATAGCTGTAGCATCCAAGGCTATG 133  
|||||  
QY 2083 CTTGGTACACTCTTCTTCCAGCTGCTCTGAGTATATGATCGAGCATGGTTGGACCAA 2142  
|||||  
Db 134 CTTTCTTACTGTGCTCTTCCAACTTTATCTGAGTATATGATCGAGAGTGGATGGACCCGG 193  
|||||  
QY 2143 TGTACTCTACACTTGGACCAATTTCAACTGGTTCCCTGTTTCTCTTACATAGCTCTCTAT 2202  
|||||  
Db 194 TGTACTTTTAAATACAGCGAAATGGTTTCTGCAATACCTTGTATTATGCTATGAT 253  
|||||  
QY 2203 CTTGTTTAGTTGAGTTTATGATTTATTTGGGTTTCAAAAGAGCTTCATGACATTAAT 2262  
|||||  
Db 254 CTCATTTTGTGGAGTTTGGAAATTTACTGGATGCAAGAGAGTTGTCATGACATAAGCCA 313  
|||||  
QY 2263 CTCCTAAGCATCTCCATGCTACCCATCATATGTACACACAGCAAAACACACTCTCTCCA 2322  
|||||  
Db 314 CTATACAACACTCTGCTGCGACCCCAACCATATTTACACAGGAGAACACCTTGTCTCCG 373  
|||||  
QY 2323 TTTTGGCGGTATGTCAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATCAATGGT 2382  
|||||  
Db 374 TTTC----- 378  
|||||  
QY 2383 GACTCTTTTACTTGATGTTTTTTCGGGTTTTTCAGGGCTCGCATTCATCCGCTGGACGGGA 2442  
|||||



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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 09:28:50 ; Search time 809 Seconds  
(without alignments)  
7927.094 Million cell updates/sec

Title: US-10-736-318-22  
Perfect score: 2925  
Sequence: 1 gtttggtatttattggtgc.....tcaaatggactaaatctg 2925

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues  
Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications NA\_New.\*
- 1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
  - 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
  - 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.2	1.9	3641	12	US-11-102-026A-181
2	53.8	1.8	305312	8	US-10-995-561-13236
3	52.8	1.8	8537	8	US-10-240-708-42
4	52	1.8	5562	8	US-10-240-708-63
5	51.6	1.8	6326	8	US-10-240-708-57
6	51.6	1.8	8607	8	US-10-240-708-72
7	51	1.7	828	6	US-09-925-065A-768903
8	50.8	1.7	664	6	US-09-925-065A-402424
9	50.8	1.7	664	6	US-09-925-065A-402425
10	50.2	1.7	5360	8	US-10-240-708-66
11	49.8	1.7	613	6	US-09-925-065A-834303
12	49.4	1.7	613	6	US-09-925-065A-834302
13	49.4	1.7	2409	8	US-10-821-234-2
14	49.4	1.7	5152	8	US-10-240-708-47
15	49.4	1.7	10166	12	US-11-147-606-3
16	49	1.7	560	6	US-09-925-065A-195994
17	49	1.7	560	6	US-09-925-065A-195995
18	49	1.7	6040	8	US-10-240-708-70
19	49	1.7	6801	8	US-10-240-708-62
20	48.8	1.7	524	6	US-09-925-065A-389544

21	48.8	1.7	562	6	US-09-925-065A-337713	Sequence 337713,
22	48.8	1.7	624	6	US-09-925-065A-749620	Sequence 749620,
23	48.8	1.7	624	6	US-09-925-065A-822274	Sequence 822274,
24	48.6	1.7	6317	8	US-10-240-708-12	Sequence 12, Appl
25	48.4	1.7	5455	8	US-10-240-708-34	Sequence 34, Appl
26	48	1.6	377	6	US-09-925-065A-599143	Sequence 599143,
27	47.8	1.6	8961	8	US-10-240-708-80	Sequence 80, Appl
28	47.6	1.6	4330	12	US-11-091-883-182	Sequence 182, App
29	47.4	1.6	6070	8	US-10-240-708-10	Sequence 10, Appl
30	47.2	1.6	1837	8	US-10-947-249-133	Sequence 133, App
31	47.2	1.6	1837	12	US-11-000-688-278	Sequence 278, App
32	47.2	1.6	5455	8	US-10-240-708-33	Sequence 33, Appl
33	47	1.6	1237	6	US-09-925-065A-714408	Sequence 714408,
34	47	1.6	1237	6	US-09-925-065A-714409	Sequence 714409,
35	47	1.6	1237	6	US-09-925-065A-714410	Sequence 714410,
36	47	1.6	1237	6	US-09-925-065A-714411	Sequence 714411,
37	47	1.6	8467	12	US-11-011-332A-96	Sequence 96, Appl
38	46.8	1.6	610	6	US-09-925-065A-939011	Sequence 939011,
39	46.8	1.6	8961	8	US-10-240-708-79	Sequence 79, Appl
40	46.8	1.6	10467	8	US-10-240-708-2	Sequence 2, Appl
41	46.8	1.6	19513	8	US-10-240-708-40	Sequence 40, Appl
42	46.6	1.6	591	6	US-09-925-065A-162822	Sequence 162822,
43	46.6	1.6	8607	8	US-10-240-708-71	Sequence 71, Appl
44	46.4	1.6	445	6	US-09-925-065A-808614	Sequence 808614,
45	46.4	1.6	8537	8	US-10-240-708-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1  
US-11-102-026A-181  
; Sequence 181, Application US/11102026A  
; Publication No. US20060021087A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; APPLICANT: Baum, James A  
; APPLICANT: Gilbertson, Larry A  
; APPLICANT: Kovalic, David K  
; APPLICANT: LaRosa, Thomas J  
; APPLICANT: Lu, Maolong  
; APPLICANT: Muniyika, Tichifa R. I.  
; APPLICANT: Roberts, James K  
; APPLICANT: Wu, Wei  
; APPLICANT: Zhang, Bei  
; TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in p1  
; FILE REFERENCE: 38-21(53596)  
; CURRENT APPLICATION NUMBER: US/11/102,026A  
; PRIOR FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: 60560842  
; PRIOR FILING DATE: 2004-04-09  
; PRIOR APPLICATION NUMBER: 60565632  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: 60579062  
; PRIOR FILING DATE: 2004-06-11  
; PRIOR APPLICATION NUMBER: 60603421  
; PRIOR FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: 60617261  
; PRIOR FILING DATE: 2004-10-11  
; PRIOR APPLICATION NUMBER: 60669241  
; PRIOR FILING DATE: 2005-04-07  
; NUMBER OF SEQ ID NOS: 190  
; SEQ ID NO 181  
; LENGTH: 3641  
; TYPE: DNA  
; ORGANISM: Lygus hesperus  
US-11-102-026A-181

Query Match 1.9%; Score 54.2; DB 12; Length 3641;  
Best Local Similarity 50.6%; Pred. No. 0.81;  
Matches 131; Conservative 0; Mismatches 128; Indels 0; Gaps 0;  
QY 1727 CCCCAAGGTACTTTTTCATTCGATGTCCTGTTTGAACCTTTCTTTTGTGATT 1786

[illegible]

```

RESULT 2
US-10-995-561-13236/c
; Sequence 13236, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13236
; LENGTH: 305312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(305312)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13236

```

```

RESULT 3
US-10-240-708-42
; Sequence 42, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 42
; LENGTH: 8537
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-240-708-42

```

RESULT 4  
US-10-240-708-63  
; Sequence 63, Application US/10240708  
; Publication No. US20050282157A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/240,708  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: FCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8



```
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 63
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-63

Query Match
Best Local Similarity 1.8%; Score 52; DB 8; Length 5562;
Matches 150; Conservative 0; Mismatches 145; Indels 1; Gaps 1;

QY 1736 TTACTTTTCAATTCGATGTTCTGTTTGAACCTTTCTTTTGTGATTCCTTCGATT 1795
D 1450 TTATATTTTATTTAGTTAGTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1509

QY 1796 GTATCCCGCATAGATGTTGTTATACGTTAAACCTTTTCTTCTACTGTTACTTCAGTTC 1855
D 1510 TTTTCTGTTAGTAGATT-TTTTCTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1568

QY 1856 TTGCTCTACTCTCATTTAATAGTTTAAAGTTTATATTTTGGCTAATCCACATT 1915
D 1569 TTATTTTATTTTGTGTTAAGAGTTTATTAATTTTATTTTATTTTATTTTATTTTAT 1628

QY 1916 TTTTAAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTCGAAATTTCT 1975
D 1629 TTAGATAGTAGTTATTTTATTTAGATTTTGTGATTAATGATTTTATTTATTTATTTAT 1688

QY 1976 GGTCTTACTTCTATTTCTGCTGTTTCTTCTATTTTGTGGTTAGAAATCCATT 2031
D 1689 TTTTGTGTTTATTTATTTATGATGTTTATTTTATTTTATTTTATTTTATTTTATTTAT 1744

RESULT 5
US-10-240-708-57
; Sequence 57, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 57
; LENGTH: 6326
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-57

Query Match
Best Local Similarity 1.8%; Score 51.6; DB 8; Length 6326;
Matches 138; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 1740 TTTTTCGAATTCGATGTTCTGTTTGAACCTTTCTTTTGTGATTCCTTCGATTCGAT 1799
D 1398 TTATTTTATTTATTTATAGTTTATTTTGTGTTTATTTTGGGTTAGTATTTATTTAGGT 1457

QY 1800 CGCCTGATAGATGTTGTTATACGTTAAACCTTTTCTTCTACTGTTACTTTTCTAGTTCTTCT 1859
D 1458 TTTTGTGTAATTTTGTGTTAGTTTATTTTGGGAGTTGTTTGTGATTTATTTATTTAT 1517

QY 1860 CTTCCTACTTCTCATTTAATAGTTTAAAGTTTAAATATTTTGGCTAATCCACATT 1919
D 1518 TTTTGTGTTTGTGTTTATTTTTCGATTTTATAGATATATTTTGTGGATTTTATTTT 1577

QY 1920 AAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATTCGAAATTCGTT 1979
D 1578 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1637

QY 1980 CTTAGTTCTATTTCTGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2021
D 1638 TCGAATTTGATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1679

RESULT 6
US-10-240-708-72
; Sequence 72, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 72
; LENGTH: 8607
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-72

Query Match
Best Local Similarity 1.8%; Score 51.6; DB 8; Length 8607;
Matches 146; Conservative 0; Mismatches 139; Indels 1; Gaps 1;

QY 1747 AATTTTCGATGTTCTGTTTGAACCTTTCTTTTGTGATTCCTTCGATTCGATTCGCTGA 1806
D 6930 AATTTGTATGTTTATGTTTATGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 6989

QY 1807 FAGATTGTTATACGTTAAACCTTTTCTTCTACTGTTACTTCTTCTTCTTCTTCTTCTAC 1866
D 6990 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 7049

QY 1867 TTCTCATTTAATAGTTTAAAGTTTAAATATTTTGGCTAATCCACATTTCGATTCGATTC 1926
D 7050 TTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 7109
```

QY 1927 ATCTTCATGAATTTGAGCTCAAAATATACCATGAA-ATTGAAATTTGGTTCCTAGT 1985  
|||  
Db 7110 ATATATTTTGTAGTAGGTTGTTGTTTGGAGAAATTAAGAGGTTTGTAGTAGTTGTG 7169  
|||  
QY 1986 TCTATTCTTGTGTTGTTCTCTATTTTGTGGTTAGAAATCCATT 2031  
|||  
Db 7170 TTGTTTGTATTTAGTTGTTTATATAGAAAGTTTATAGAAATAGTT 7215  
|||

## RESULT 7

US-09-925-065A-768903  
; Sequence 768903, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 768903  
; LENGTH: 628  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-768903

Query Match 1.7%; Score 51; DB 6; Length 628;

Best Local Similarity 51.7%; Pred. No. 2;  
Matches 140; Conservative 1; Mismatches 126; Indels 4; Gaps 1;  
QY 1654 GAAACATACCTACTCTCATCTCCGGCTTCTCTGGTCTTCTACATCTATTACCTTAAAC 1713  
|||  
Db 353 GTAATGATCAATTTTCAAGTCGACTTTATGTAATCAATGCTCTCTATTAATTTTAT 412  
|||  
QY 1714 TCAAGCTTTACGTCCTCCAAAGGTACTTTTTTCAATTTGATGTTCTGTTTGAACCTT 1773  
|||  
Db 413 TTTTAGTGTAGCTCGGCTAAAAGTTTCTATTTGTTTATCTTTGCTTCATTGA---TA 468  
|||  
QY 1774 TCTTTTGTGATTCCTTCGATGTTGATCGGCTGATAGATGTTGTTATACGTTAACCTTTT 1833  
|||  
Db 469 TTTTGTATGTTTCTTGTGTTTAAATTTCAATTTATTTCTGCTCTGATCTTTATTTGT 528  
|||  
QY 1834 TCTTACTGTACTTTTCAGTCTTGCTCTCTACTCTCTCATTTAATAGTTTAAAGTTTA 1893  
|||  
Db 529 TTTCTTCTACTAATTTGGGTTAGTTGTTGTTGTTGTTTCTTAACTTCTTAAATGATC 588  
|||  
QY 1894 ATATTTTGGCTAATCCACATTTTAAAGTT 1924  
|||  
Db 589 ATAAAGTTGTTCAATGAAAGTTTCTTACTT 619  
|||

## RESULT 8

US-09-925-065A-402424/c  
; Sequence 402424, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 402424  
; LENGTH: 664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-402424

Query Match 1.7%; Score 50.8; DB 6; Length 664;

Best Local Similarity 48.0%; Pred. No. 2.2; Mismatches 153; Indels 0; Gaps 0;  
Matches 142; Conservative 1;  
QY 1736 TTACTTTTTTCAATTTTCGATGTTCTGTTTGAACCTTTCTTTGTTGATTCCTTCGATT 1795  
|||  
Db 462 TGACTTTTCAAAAACCAATTTTGTGTTGATCTTTTGTATTTTCTTTTCTTTAAAT 403  
|||  
QY 1796 GATCGCCTGATAGATTGTTATAGTTAACCTTTTCTTCTACTGTTACTTTCAGTTTC 1855  
|||  
Db 402 TCAATTTTCAATTTTCTGTCGACCTTTATTTTTTCTTCTACTAAATTTTGGGTT 343  
|||  
QY 1856 TTGCTCTTCTACTTCTCAATTTAATAGTTTAAAGTTTAAATATTTTGGCTAATCCACAT 1915  
|||  
Db 342 TCGTTTGGCTCTTGCATTTCTAGTTCTTTAAGATGATCATAGATGTTTATTTAAAT 283  
|||  
QY 1916 TTTTAAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAAATGAAATTTGT 1975  
|||  
Db 282 TTTTCTCTTTTGTGATGATAGACATATATAGCTATAAATTTCCCTCTTCTAGTTCTGCTTTG 223  
|||  
QY 1976 GGTCTTAGTTCTATTTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2031  
|||  
Db 222 TGTATCTCAAGGTTTAAATACGTCATGTTTCCATTTATCATTTGTTTCAAGAAAT 167  
|||

## RESULT 9

US-09-925-065A-402425/c  
; Sequence 402425, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 402425  
; LENGTH: 664  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-402425

Query Match 1.7%; Score 50.8; DB 6; Length 664;  
Best Local Similarity 48.0%; Pred. No. 2.2;  
Matches 142; Conservative 1; Mismatches 153; Indels 0; Gaps 0;

QY 1736 TTACTTTTTCATTTTCGATGTTCTGTTTGAACCTTTCTTTTGTGATCTCTTCGATT 1795  
DB 462 TGACITTTTCAAAACCCAAATTTTGTGTTGCTGATCTTTGATTTTCTTTTAAAT 403

QY 1796 GTATCGCTGATAGATGTTGTATAGCTTAACCTTTTCTTACTGTTACTTTCAGTTC 1855  
DB 402 TCAATTTTATTTATTTCTGTCGACCTTTATTTTCTTCTACTAAATTTGGGT 343

QY 1856 TTGCTCTTACTTCTCATTTAATAGTTTAAAGTTTAAATTTTGGCTAAATCCACATT 1915  
DB 342 TGCTTTGCTCTTGCAATTTCTAGTTCTTTAAGATGCATCATTTAGTTTATTTAAAT 283

QY 1916 TTTTAAAGTTGAATCTTCCATGAATTTGAGCTCAAAATATACCATGAATGAAATTTGT 1975  
DB 282 TTTTCTCTTTTGTGATGACACTTATAGCTATAAATTCCTCTTAGTCTGCTTTTG 223

QY 1976 GGTCTTCTAGTTCTATTTCTGTTGTTTCTTCTATTTTGTGTTAGATCCATT 2031  
DB 222 TGTATCTCAAGTTTAAATAGCTCATGTTTCCATATCATTTGTTTCAAGAAAT 167

RESULT 10  
US-10-240-708-66  
; Sequence 66, Application US/10240708  
; Publication No. US20050282157A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/240,708  
; PRIOR FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 66  
; LENGTH: 5360  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-708-66

Query Match 1.7%; Score 50.2; DB 8; Length 5360;  
Best Local Similarity 47.3%; Pred. No. 5.2; Mismatches 168; Indels 0; Gaps 0;  
Matches 151; Conservative 0

QY 1744 TTCAATTTTCGATGTTCTGTTTGAACCTTTCTTTTGTGATTCCTTCGATGTTATCGCC 1803  
DB 14 TTGTTTTTTTTTATTTGTTATAAAGATTTTATATTTTGTGTTATGTTTACGGTTTA 73

QY 1804 TGATAGATTGTTGTTACGTTAACTTTTCTTACTGTTTACTTTTCAGTTCTTTCCTTC 1863  
DB 74 TTTTAAATTTATTTGTTTATTTTATTTTGTTTTAAATTTATAGAAATATTGTAGTTA 133

QY 1864 TACTTCTCATTTAATAGTTTAAAGTTTAAATTTTGGCTAAATCCAAATTTTAACT 1923  
DB 134 TTTAAATAGTTATGTTTGTGTTTAAATTTAGAAATTTATGTTATTTTCGATTTGTTTCGTTT 193

QY 1924 TGAATCTTCCATGAAATTTGAGCTCAAAATATATACCATGAAATTTGAAATTTGTTGTTCTTA 1983  
DB 194 TGAATGTTTATTTTGTGTTTAAATTTATTTTAAATGTTTGTGAAATTTTATGTTATTTT 253

QY 1984 GTTCTATTTCTGCTTCTGTTTCTTCTATTTTGTGTTAGATCCATTTCTACGAGAAAG 2043  
DB 254 TTTTGTGTTATTTTATGATGTTTCGTTTTTTTAAATGATTAATAAATTTTGTGTTAATATG 313

QY 2044 GCAATGCTTTTGCATAATAT 2062  
DB 314 TAAATTTTATAGTAGTTT 332

RESULT 11  
US-09-925-065A-834303  
; Sequence 834303, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 834303  
; LENGTH: 613  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-834303

Query Match 1.7%; Score 49.8; DB 6; Length 613;  
Best Local Similarity 51.7%; Pred. No. 3.3;  
Matches 140; Conservative 0; Mismatches 127; Indels 4; Gaps 1;

QY 1654 GAAACATATCTTACTTCTCATCTCGGCTTCTCTGCTTCTTACATCTATTTACCTTAAAC 1713  
DB 5 GTAATGTTATCATTTTTCATGCTGACTTTATGTAATTCAAATGTCTCTATTAATTTTAT 64

QY 1714 TCAACGTTTACGTCCCAAGGTTACTTTTTTCAATTTTCGATGTTCTGTTTGAACCTT 1773  
DB 65 TTTTATGTTAGTCTGCTGCTAAAGTTTTCATTTTGTATCTTTGCTTCAATGA---TA 120

QY 1774 TCTTTTGTGATTCCTTCGATTTGATCGCTGATAGATGTTGTTATACGTTAACCTTTT 1833  
DB 121 TTTTGTATGTTTCTTCTTGTGTTTAAATTTCAATTTATTTCTGCTCTCATTTATTGTT 180

QY 1834 TTTCTACTGTTTACTTTTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1893  
DB 181 TTTCTTCTACTAAATTTGCGTTTGTGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240

QY 1894 ATATTTTGGCTTAATCCACATTTTAAAGTT 1924  
DB 241 ATAAATGTTTCAATTTGAAGTTTCTACTT 271

RESULT 12  
US-09-925-065A-834302  
; Sequence 834302, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.

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; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 834302
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-834302
```

```
Query Match 1.7%; Score 49.4; DB 6; Length 613;
Best Local Similarity 51.3%; Pred. No. 4;
Matches 139; Conservative 1; Mismatches 127; Indels 4; Gaps 1;

QY 1654 GAAACATCTCTACTCACTCGGCTTCTCGGTCTTACATCTATTACCTTAAC 1713
DB 5 GTAATGTATCATTTTTCATGCTGACTTTATGTAATTCAAATGCTCTATTATTTTAT 64

QY 1714 TCAACGTTTACGCCCAAGGTACTTTTTCATTTTCGATCTCTGTTTGAACCTT 1773
DB 65 TTTTAGTAGCTGGCTAAAGTTTTTCTAATTTGTTATCTTGTCTCAATGA----TA 120

QY 1774 TCTTTTGTGATTCCTTCGATTCATCGCTGATAGATGTGTATACGTTAACCTTTT 1833
DB 121 TTTTGTATGTTTCTTGTGTTAAATTCATTTATTTCTGCTGATCTTATATTGCT 180

QY 1834 TCTTACTGTACTTTCAGTCTTGTCTTCTACTCTCAATTAATTAAGTTTAAAGTTT 1893
DB 181 TTTCTTCTACTAATTTTGGGTTTGTGTTCTGCTTTTCTAATTTCTTAAATGCATC 240

QY 1894 ATATTTTGTGCTAATCCACATTTTAAAGTT 1924
DB 241 ATAAAGTTGTTCAATGAAGTTTTCCTACTT 271
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RESULT 13
US-10-821-234-2/c
; Sequence 2, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 2
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-2
```

```
Query Match 1.7%; Score 49.4; DB 8; Length 2409;
Best Local Similarity 50.6%; Pred. No. 5.9;
```

```
Matches 119; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2317 TCTCCATTTGCCGGTATGTCAAAAGCTATATGTTCTCAATCTAAATTTCAAGAGCTTGTATC 2376
DB 1413 TGTTCATCTACTGGATTCACAGAGCCTTCACTATAGACTGGTATATAGCGGCTACATA 1354

QY 2377 AATGGTGACTTCTTTTACTTTGATGTTTTTGGGGTTTTCAGGGCTCGCATTCCTCCCTGG 2436
DB 1353 NACCTCACCATATTTGGAAGATTCCTACTCCATTTGCAAGTCATGCTTTTCACCCCTATTG 1294

QY 2437 ACGGATACTTCAGGCTATACCGCAGCTGATAGCGTGTATAGTGGCGATTCATCTCA 2496
DB 1293 ATGGCTTTCTTCAGAGTCTACCTTACCATATATACCCCTTTTATCTTCTCCATTACACAAG 1234

QY 2497 TAAACATCTGAGTCTTTTGTGTTTGGAGGGATATGGACAGCAAGCATCCCATGA 2551
DB 1233 TGGTTTATTAAAGTCTGTACATCTCTGGTTAATATCTGGAACAATTTCCATTTCATGA 1179
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```
RESULT 14
US-10-240-708-47
; Sequence 47, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 47
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (67, 2620)
US-10-240-708-47
```

```
Query Match 1.7%; Score 49.4; DB 8; Length 5152;
Best Local Similarity 50.4%; Pred. No. 7.3;
Matches 119; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 1736 TTACTTTTTTCAATTTTCGATGTTGTTTGAACCTTCTTTTGTGATTCCTTCGATT 1795
DB 7 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 66

QY 1796 GTATCGCCTGATAGATTGTTTATACGTTTAACTTTTCTTACTGTTTACTTTCAGTTC 1855
DB 67 NTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 126

QY 1856 TTGTCCTTCTACTCTCTCAATTAATAGTTTTTAAAGTTTAAATATATTTTGGCTAATFCCAATT 1915
DB 127 TTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATTTAGGAGATTAAAGTGTAGTAGT 186

QY 1916 TTTTAAAGTTGAATCTTCCATGAAATTTGAGCTCAAAATATACCATGAATTTGAAT 1971
DB 187 TATGATCGTGTATTGTAATTTAGTTTGGGTAATAAAGTAAGATTTTGTGTTTAAAT 242
```

```
RESULT 15
US-11-147-606-3
; Sequence 3, Application US/11147606
; Publication No. US20050278795A1
; GENERAL INFORMATION:
; APPLICANT: Ntambi, James M.
; TITLE OF INVENTION: Stearoyl-CoA desaturase 4 gene
; FILE REFERENCE: 960296.00197
; CURRENT APPLICATION NUMBER: US/11/147,606
; PRIOR FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: 60/578,234
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 10166
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-147-606-3

Query Match      1.7%; Score 49.4; DB 12; Length 10166;
Best Local Similarity 49.4%; Pred. No. 8.9;
Matches 128; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 775 GAGTGAGATGCCACTGGGTTTGGTCTCTCTCTCTCTCTCTCTCAACCTT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7902 GAGATGGACTTGCAAACTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG 7961

QY 835 AGTTTCAGCCTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7962 TTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTT 8021

QY 895 TCCAATTATATTGTACAAACATTTGCTCTAGTTTAAACATGTAAATGTTGATGAT 954
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8022 TTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTT 8081

QY 955 CTTTGCAAGACTCCATTTTGTAAAGTAAACCTTGAATCTCATAGATTGCGATTGTT 1014
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8082 TTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGTGGTTTGT 8141

QY 1015 GGTATTTCATTTCAGGT 1033
   ||| ||| ||| ||| |||
Db 8142 GGTATTTCAGGT 8160
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Search completed: March 7, 2006, 09:42:29  
Job time : 811 secs

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